


```

PR 18-OCT-1994; 94JP-0252166.
PR 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
XX N-PSDB; AAT38628.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 30; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
XX monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
XX combining light and heavy variable region DNA, from a murine
XX anti-human myeloblastoma cell Mab, with human light and heavy
XX constant region sequences, respectively to produce chimaeric
XX human/murine light and heavy chain DNA mols.. A recombinant vector
XX for the expression of the heavy and light chain DNA mols. was
XX prepd., and used to transform a host cell. The host cell was then
XX cultured, and the expression prods. of the heavy and light chain
XX DNA mols. sepd. and connected with a peptide linker to produce a
XX single stranded Fv region. The reshaped Fv region has low human
XX antigenicity, and is therefore expected to be useful as an agent
XX for the diagnosis and treatment of cerebral tumours,
XX e.g. myeloblastoma.
XX
XX Sequence 126 AA:
SQ

```

Query Match 92.7%; Score 518; DB 17; Length 126;
Best Local Similarity 93.5%; Pred. No. 4.3e-31;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

```

QY 1 DIQMTQSSPSLSASVGDRTYTCRKSQNVGTWAWYQOKPKGAPRLIYSASFLLSGVPY 60
   |||
Db 20 dlmqtqspsslsasvgydrvtltckasqngvtnvaygqkpkapkllysaasyrysgyps 79
   |||
QY 61 RFGSGSGTDFLTITSSLOPEFATYCCQVNYIVPLTFGCGKVEIK 107
   |||
Db 80 rfsqsgsgtdfltlisslqpediatlycqqynspratfsgtkveik 126
   |||

```

RESULT 2
AA556680
ID AA556680 standard; protein: 107 AA.
XX
XX AA556680;
XX
XX 15-FEB-2000 (first entry)
XX
XX Anti-erythropoietin receptor Mab 3G9 light chain variable region.
XX
XX Complementarity determining region; antibody; primate; immunogenicity;
XX Old World ape; Old World monkey; antigen-binding affinity.
XX
XX Synthetic.
XX Mus sp.
XX Pan troglodytes.
XX
XX MO9955369-A1.
XX
XX 04-NOV-1999.
XX
XX 28-APR-1999; 99WO-US09131.
XX
XX 28-APR-1998; 98US-0083367.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Taylor AH;
PI

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XX
XX WPI: 2000-023265/02.
XX
XX Antibodies containing donor complementarity determining regions and
XX non-human primate acceptor frameworks, having reduced immunogenicity in
XX humans -
XX
XX Example 8; Page 114-115; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
XX (complementarity determining regions) derived from a non-human antigen-
XX specific donor antibody, and an acceptor framework from a non-human
XX primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX specific donor antibody onto homologous Old World ape or monkey acceptor
XX frameworks. The Abs have reduced immunogenicity and are better tolerated
XX in humans (because of the close similarity between the human and primate
XX proteins), but retain the full antigen-binding affinity of the donor
XX antibody.
XX
XX Sequence 107 AA:
SQ

```

Query Match 92.1%; Score 515; DB 21; Length 107;
Best Local Similarity 93.5%; Pred. No. 6.2e-31;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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QY 1 DIQMTQSSPSLSASVGDRTYTCRKSQNVGTWAWYQOKPKGAPRLIYSASFLLSGVPY 60
   |||
Db 1 dlmqtqspsslsasvgydrvtltckasqngvtnvaygqkpkapkllysaasyrysgypd 60
   |||
QY 61 RFGSGSGTDFLTITSSLOPEFATYCCQVNYIVPLTFGCGKVEIK 107
   |||
Db 61 rfsqsgsgtdfltlisslqpediatlycqqynspratfsgtkveik 107
   |||

```

RESULT 3
AAR76665
ID AAR76665 standard; protein: 126 AA.
XX
XX AAR76665;
XX
XX 17-JAN-1996 (first entry)
XX
XX Human/murine chimeric antibody HEF-RVL-M21a-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21a-g kappa;
XX medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
XX 1..19
XX /label= sig_peptide
XX 20..43
XX /label= FR 1
XX 44..54
XX /label= CDR 1
XX 55..69
XX /label= FR 2
XX 70..76
XX /label= CDR 2
XX 77..108
XX /label= FR 3
XX 109..117
XX /label= CDR 3
XX 118..126
XX /label= FR 4
XX
XX MO9514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX

[illegible]

FT	Peptide	118..126
FT		/label= FR 4
PN	WO9514041-A1.	
XX		
XX	26-MAY-1995.	
PD		
XX	19-OCT-1994;	94WO-JP01763.
PE		
XX	19-NOV-1993;	93JP-0291078.
PR		
XX	(CHUS) CHUGAI SEIYAKU KK.	
PA		
XX	Ohtomo T, Sato K, Tsuchiya M;	
PI		
DR	WPI; 1995-200347/26.	
XX		
PT	Reconstituted antibody against human medullo:blastoma cells -	
PT	contains high proportion of human antibody origin and has low	
PT	antigenicity	
XX		
PS	Claim 33; Page 66; 120pp; Japanese.	
XX		
CC	AA094502 encodes AAR76666 the human/murine chimeric antibody HEF-	
CC	RV-M21b-g kappa. The antibody is reactive with human medullo-	
CC	blastoma (a brain tumour) cells. The chimeric antibody can be	
CC	used in the diagnosis and treatment of this disease.	
CC		
XX	Sequence 126 AA;	
SO		
Query Match	91.4%; Score 511; DB 16; Length 126;	
Best Local Similarity	91.6%; Pred. No. 1.4e-30;	
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;		
OY	1 DIOMTSPSSLSASVGDRTITRCASONVGTWAWYOOKPKGAPKILLYSASFLYSGVPY 60	
DB	20 diqmctqspsslsasvqdvrtltckasqngvavayqdkpypakpalllysasrysgyps 79	
OY	61 RFGSGSGTDFLTRITRISLOPEDFATRYCOQYNIYPLTREGGTRVEIK 107	
DB	80 rfsgsgsgtdyftlrlslsqpedialrycqgynsyprafsgyglkveik 126	
RESULT 6		
AAW04381		
ID	AAW04381 standard; Protein; 126 AA.	
XX		
AC	AAW04381;	
XX		
DT	09-DEC-1996 (first entry)	
XX		
DE	Chimaeric human/murine MAB ONS-M21 fragment HEF-RVL-M21b-g(kappa).	
XX		
KW	Murine; human; myeloblastoma; chimaera; monoclonal antibody;	
KW	chimaera; single stranded Fv region; low human antigenicity;	
KW	diagnosis; treatment; cerebral tumour; reshaped.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= sig_peptide
FT	Peptide	20..125
FT		/label= mat_peptide
FT	Region	33..53
FT		/label= CDR_1
FT	Region	69..75
FT		/label= CDR_2
FT	Region	108..116
FT		/label= CDR_3
XX		
XX	JP08169900-A.	

[illegible]

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FT      /label= FR 2
FT      Peptide 70..76
FT      /label= CDR_2
FT      Peptide 77..108
FT      /label= FR_3
FT      Peptide 109..117
FT      /label= CDR_3
FT      Peptide 118..126
FT      /label= FR_4
XX
XX      WO9514041-A1.
XX
XX      26-MAY-1995.
XX
XX      19-OCT-1994; 94MO-JP01763.
XX
XX      19-NOV-1993; 93JP-0291078.
XX
XX      (CHUS ) CHUGAI SEIYAKU KK.
XX
XX      Ohtomo T, Sato K, Tsuchiya M;
XX
XX      WPI; 1995-200347/26.
XX      N-PSDB; AAQ94505.
XX
XX      Reconstituted antibody against human medulloblastoma cells -
XX      contains high proportion of human antibody origin and has low
XX      antigenicity
XX
XX      Claim 33; Page 68; 120pp; Japanese.
XX
XX      AAQ94505 encodes AAR76667 the human/murine chimeric antibody HEF-
XX      RVL-M21c-g kappa. The antibody is reactive with human medullo-
XX      blastoma (a brain tumour) cells. The chimeric antibody can be
XX      used in the diagnosis and treatment of this disease.
XX
XX      Sequence 126 AA;

Query Match 91.2%; Score 510; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.6e-30;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 DIQMTQSSLSASVGRVITTCASQNVGNVAMYOQKPKAPKLLIYSASFYSGVPY 60
DB      20 dIqmtqspsslsasvgrvlttcasqnvgnvawyqkpkapKLLIYSAsYrYsgvps 79
QY      61 RFSGSGSGTDFTLTISSLPEDFATYYCOQYNITPLTFGGGKVEIK 107
DB      80 rfsgsgsgtdftltisslpediatyfcqgynsyprafgqgtkveik 126

RESULT 8
AA04382
ID      AA04382 standard; Protein; 126 AA.
XX
XX      AA04382;
XX
XX      09-DEC-1996 (first entry)
XX
XX      Chimaeric human/murine Mab ONS-M21 fragment HEF-RVL-M21c-g(kappa).
XX
XX      Murine; human; myeloblastoma; chimaera; monoclonal antibody;
XX      chimera; single stranded Fv region; low human antigenicity;
XX      diagnosis; treatment; cerebral tumour; reshaped.
XX
XX      Synthetic.
XX
XX      key Location/Qualifiers
XX      Peptide 1..19
XX      /label= sig_peptide
XX      Peptide 20..125
XX      /label= mat_peptide

```

```

FT      Region 33..53
FT      /label= CDR_1
FT      Region 69..75
FT      /label= CDR_2
FT      Region 108..116
FT      /label= CDR_3
XX
XX      JP08169900-A.
XX
XX      02-JUL-1996.
XX
XX      18-NOV-1994; 94JP-0285057.
XX
XX      18-OCT-1994; 94JP-0252166.
XX      19-NOV-1993; 93JP-0291078.
XX
XX      (CHUS ) CHUGAI PHARM CO LTD.
XX
XX      WPI; 1996-358509/36.
XX      N-PSDB; AAT38619.
XX
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
XX      human antigenicity, and is therefore useful for diagnosis and
XX      treatment of cerebral tumours, e.g. myeloblastoma
XX
XX      Example 5; Page 26; 45pp; Japanese.
XX
XX      The present sequence is a fragment of the chimaeric human/murine
XX      monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
XX      combining light and heavy variable region DNA, from a murine
XX      anti-human myeloblastoma cell Mab, with human light and heavy
XX      constant region sequences, respectively to produce chimeric
XX      human/murine light and heavy chain DNA mols.. A recombinant vector
XX      for the expression of the heavy and light chain DNA mols. was
XX      prepd., and used to transform a host cell. The host cell was then
XX      cultured, and the expression prods. of the heavy and light chain
XX      DNA mols. sepd. and connected with a peptide linker to produce a
XX      single stranded Fv region. The reshaped Fv region has low human
XX      antigenicity, and is therefore expected to be useful as an agent
XX      for the diagnosis and treatment of cerebral tumours,
XX      e.g. myeloblastoma.
XX
XX      Sequence 126 AA;

Query Match 91.2%; Score 510; DB 17; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.6e-30;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 DIQMTQSSLSASVGRVITTCASQNVGNVAMYOQKPKAPKLLIYSASFYSGVPY 60
DB      20 dIqmtqspsslsasvgrvlttcasqnvgnvawyqkpkapKLLIYSAsYrYsgvps 79
QY      61 RFSGSGSGTDFTLTISSLPEDFATYYCOQYNITPLTFGGGKVEIK 107
DB      80 rfsgsgsgtdftltisslpediatyfcqgynsyprafgqgtkveik 126

RESULT 9
AAR76669
ID      AAR76669 standard; Protein; 126 AA.
XX
XX      AAR76669;
XX
XX      17-JAN-1996 (first entry)
XX
XX      Human/murine chimeric antibody HEF-RVL-M21c-g kappa.
XX
XX      Human; murine; chimeric antibody; HEF-RVL-M21c-g kappa;
XX      medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX      Homo sapiens.

```

Key	Location/Qualifiers
FT Peptide	1..19
FT Peptide	/label= sig-peptide
FT Peptide	20..43
FT Peptide	/label= FR 1
FT Peptide	44..54
FT Peptide	/label= CDR 1
FT Peptide	55..69
FT Peptide	/label= FR 2
FT Peptide	70..76
FT Peptide	/label= CDR 2
FT Peptide	77..108
FT Peptide	/label= FR 3
FT Peptide	109..117
FT Peptide	/label= CDR 3
FT Peptide	118..126
FT Peptide	/label= FR 4
PN W09514041-A1.	
PD 26-MAY-1995.	
PF 19-OCT-1994;	94WO-JP01763.
PR 19-NOV-1993;	93JP-0291078.
PA (CHUGAI) CHUGAI SEIYAKU KK.	
PI Ohtomo T, Sato K, Tsuchiya M;	
PI WPI: 1995-200347/26.	
DR N-PSDB; AA094509.	
XX Reconstituted antibody against human medulloblastoma cells -	
XX contains high proportion of human antibody origin and has low	
XX antigenicity	
PS Claim 33; Pages 71-72; 120pp; Japanese.	
XX AA094509 encodes AAR76669 the human/murine chimeric antibody HEF-	
XX RVL-M21e-g kappa. The antibody is reactive with human medullo-	
XX blastoma (a brain tumour) cells. The chimeric antibody can be	
XX used in the diagnosis and treatment of this disease.	
XX Sequence 126 AA;	
SO	
Query Match	91.1%; Score 509; DB 16; Length 126;
Best Local Similarity	90.7%; Pred. No. 1.9e-30;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;	
OY 1 DIQMTQSPSSLSASVGDRVTITCKASQNYGTWAWYQOKPKGAPKLLIYSASFLYSGVPY 60	
DB 20 dltqmtqspsslsasvgydrsvctskasqnygtvawvayqgkpkapkllysaasyrysgvps 79	
OY 61 RFSSGSGSGTDEFTLTITSSLDPEDFATRYCOQYNIYPLTFSGGTVEIK 107	
DB 80 rfsfgsgsgtdftltitssldpeditatrycqqynsyprafgqgtkveik 126	
RESULT 10	
AAR76671	
ID AAR76671 standard; Protein: 126 AA.	
AC AAR76671;	
XX 17-JAN-1996 (first entry)	
DT Human/murine chimeric antibody HEF-RVL-M21g-g kappa.	
XX Human; murine; chimeric antibody; HEF-RVL-M21g-g kappa;	
KM medulloblastoma; brain tumour; treatment; diagnosis.	
XX	

OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Pepptide 1..19 /label= sig_peptide
FT	Pepptide 20..43 /label= FR 1
FT	Pepptide 44..54 /label= CDR 1
FT	Pepptide 55..69 /label= FR 2
FT	Pepptide 70..76 /label= CDR 2
FT	Pepptide 77..108 /label= FR 3
FT	Pepptide 109..117 /label= CDR 3
FT	Pepptide 118..126 /label= FR 4
PN	WO9514041-A1.
PD	26-MAY-1995.
PR	19-OCT-1994; 94WO-JP01763.
PA	(CHUS) CHUGAI SEIYAKU KK.
PI	Ohtomo T, Sato K, Tsuchiya M;
WPI:	1995-200347/26.
N-PSDB:	AAG94513.
Reconstituted antibody against human medulloblastoma cells - contains high proportion of human antibody origin and has low antigenicity	
Claim 33; Page 75; 120pp; Japanese.	
AAG94513 encodes AAR76671 the human/murine chimeric antibody HEF-RVL-M21g-g kappa. The antibody is reactive with human medullo-	
blastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.	
Sequence 126 AA:	
Query Match Best Local Similarity Matches 97; Conservative 91.1%; Score 509; DB 16; Length 126; Pred. No. 1.9e-30; Indels 0; Gaps 0.	
DQYMSPSSISASVGDRTITCKAQNNGTVAWMGKPKAPKLIIYSASEIVSGVPY 60 : : : : DQDMQGSPSSIASAVGYDVSVTCASGVNVAWGYPKPGLIKLIIYSASYRGVS 79 : : : :	
RFSGGSCGTDFLTITSLOPEDFAFYVCQOYNIPPLTFEGCGTKVEIK 107 : : : :	
rfsqsgstcftltsisigpediatyfcggynsyprafsgglkveik 126	
RESULT 11	
ID AAM04384 standard; Protein; 126 AA.	
AAM04384;	
AC AC	
DT DT	09-DEC-1996 (first entry)
DE Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21e-g(kappa).	
Mutrine; human; myeloblastoma; chimaira; monoclonal antibody;	

```
KW chimera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig-peptide
FT Peptide 20..125
FT /label= mat-peptide
FT Region 33..53
FT /label= CDR_1
FT Region 69..75
FT /label= CDR_2
FT Region 108..116
FT /label= CDR_3
FT Region /label= CDR_3
PN JP08169900-A.
PD 02-JUL-1996.
XX
XX 18-NOV-1994; 94JP-0285057.
XX
XX 18-OCT-1994; 94JP-0252166.
PR 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
DR N-PSDB; AAT38623.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Pages 27-28; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
CC monoclonal antibody (MAb) ONS-M21. The MAb was prep'd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell MAb, with human light and heavy
CC constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prep'd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sep'd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
XX Sequence 126 AA:
SQ
Query Match 91.1%; Score 509; DB 17; Length 126;
Best Local Similarity 90.7%; Pred. No. 1.9e-30;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNAVYQOKPGKAPKLLIYSASFYSGVPY 60
DB 20 diqmtqspsslsasvgrvsvtkcasqngvtnvaygqkpgkpklllysasrysgvps 79
QY 61 RFSGSGGTFTLTLSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
DB 80 rfsgsggtftltlsslqpediatyfcgqynsyprafggtkveik 126
```

```
RESULT 12
AAW04386
ID AAW04386 standard; Protein; 126 AA.
XX
AC AAW04386;
```

```
XX
DT 09-DEC-1996 (first entry)
XX
DE Chimaeric human/murine MAb ONS-M21 fragment HFE-RVL-M21g-g(kappa).
XX
XX Murine; human; myeloblastoma; chimera; monoclonal antibody;
KW chimera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig-peptide
FT Peptide 20..125
FT /label= mat-peptide
FT Region 33..53
FT /label= CDR_1
FT Region 69..75
FT /label= CDR_2
FT Region 108..116
FT /label= CDR_3
FT Region /label= CDR_3
PN JP08169900-A.
PD 02-JUL-1996.
XX
XX 18-NOV-1994; 94JP-0285057.
XX
XX 18-OCT-1994; 94JP-0252166.
PR 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
DR N-PSDB; AAT38627.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Pages 29-30; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
CC monoclonal antibody (MAb) ONS-M21. The MAb was prep'd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell MAb, with human light and heavy
CC constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prep'd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sep'd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
XX Sequence 126 AA:
SQ
Query Match 91.1%; Score 509; DB 17; Length 126;
Best Local Similarity 90.7%; Pred. No. 1.9e-30;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNAVYQOKPGKAPKLLIYSASFYSGVPY 60
DB 20 diqmtqspsslsasvgrvsvtkcasqngvtnvaygqkpgkpklllysasrysgvps 79
QY 61 RFSGSGGTFTLTLSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
DB 80 rfsgsggtftltlsslqpediatyfcgqynsyprafggtkveik 126
```

```
RESULT 13
AAR76672
ID AAR76672 standard; Protein: 126 AA.
XX
AC AAR76672;
XX
DT 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21h-g kappa.
XX
KW Human; murine; chimeric antibody; HEF-RVL-M21h-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..43
FT Peptide /label= FR 1
FT Peptide 44..54
FT Peptide /label= CDR 1
FT Peptide 55..69
FT Peptide /label= FR 2
FT Peptide 70..76
FT Peptide /label= CDR 2
FT Peptide 77..108
FT Peptide /label= FR 3
FT Peptide 109..117
FT Peptide /label= CDR 3
FT Peptide 118..126
FT Peptide /label= FR 4
XX
PN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PE 19-OCT-1994; 94WO-JP01763.
XX
PR 19-NOV-1993; 93JP-0291078.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
XX
DR WPI: 1995-200347/26.
DR N-PSDB: AAQ94514.
XX
PT Reconstituted antibody against human medullo:blastoma cells -
PT contains high proportion of human antibody origin and has low
PT antigenicity
XX
PS Claim 33; Pages 76-77; 120pp; Japanese.
XX
CC AAQ94514 encodes AAR76672 the human/murine chimeric antibody HEF-
CC RVL-M21h-g kappa. The antibody is reactive with human medullo-
CC blastoma (a brain tumour) cells. The chimeric antibody can be
CC used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA:

Query Match 90.9%; Score 508; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.3e-30;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
```

```
Db 80 rftsgsgstdflltllssldpediatlcygcqgynsprafggtkveik 126
RESULT 14
AAR76680
ID AAR76680 standard; Protein: 126 AA.
XX
AC AAR76680;
XX
DT 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21p-g kappa.
XX
KW Human; murine; chimeric antibody; HEF-RVL-M21p-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..43
FT Peptide /label= FR 1
FT Peptide 44..54
FT Peptide /label= CDR 1
FT Peptide 55..69
FT Peptide /label= FR 2
FT Peptide 70..76
FT Peptide /label= CDR 2
FT Peptide 77..108
FT Peptide /label= FR 3
FT Peptide 109..117
FT Peptide /label= CDR 3
FT Peptide 118..126
FT Peptide /label= FR 4
XX
PN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PE 19-OCT-1994; 94WO-JP01763.
XX
PR 19-NOV-1993; 93JP-0291078.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
XX
DR WPI: 1995-200347/26.
DR N-PSDB: AAQ94532.
XX
PT Reconstituted antibody against human medullo:blastoma cells -
PT contains high proportion of human antibody origin and has low
PT antigenicity
XX
PS Claim 24; Pages 90-91; 120pp; Japanese.
XX
CC AAQ94532 encodes AAR76680 the human/murine chimeric antibody HEF-
CC RVL-M21p-g kappa. The antibody is reactive with human medullo-
CC blastoma (a brain tumour) cells. The chimeric antibody can be
CC used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA:

Query Match 90.7%; Score 507; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.7e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
```


QY 61 RFGSGSGTDFTLTISLQEPEDFATYCCOYNIYPLTFGGGTKEIK 107
 |||||||
 DB 80 rfgsgsgtdftltisslqepediatyccqynsyprafggtkveik 126

RESULT 15

AAR76678
 ID AAR76678 standard: Protein: 126 AA.

AC AAR76678;

DT 17-JAN-1996 (first entry)

DE Human/murine chimeric antibody HEF-RVL-M21n-g kappa.

KW Human; murine; chimeric antibody; HEF-RVL-M21n-g kappa;
 medulloblastoma; brain tumour; treatment; diagnosis.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..19
 /label= sig_peptide

FT Peptide 20..43
 /label= FR 1

FT Peptide 44..54
 /label= CDR 1

FT Peptide 55..69
 /label= FR 2

FT Peptide 70..76
 /label= CDR 2

FT Peptide 77..108
 /label= FR 3

FT Peptide 109..117
 /label= CDR 3

FT Peptide 118..126
 /label= FR 4

PN W09514041-A1.

XX 26-MAY-1995.

XX 19-OCT-1994; 94WO-JP01763.

XX 19-NOV-1993; 93JP-0291078.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ohtomo T, Sato K, Tsuchiya M;

XX WPT: 1995-200347/26.

XX N-PSDB: AAO94528.

XX Reconstituted antibody against human medullo:blastoma cells -
 contains high proportion of human antibody origin and has low
 antigenicity

XX Claim 33; Page 87; 120pp; Japanese.

XX AA094528 encodes AAR76678 the human/murine chimeric antibody HEF-
 RVL-M21n-g kappa. The antibody is reactive with human medullo-
 blastoma (a brain tumour) cells. The chimeric antibody can be

XX used in the diagnosis and treatment of this disease.

XX SQ Sequence 126 AA;

Query Match 90.7%; Score 507; DB 16; Length 126;

Best Local Similarity 90.7%; Pred. No. 2.7e-30; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLASVGDRTVITCKASQNVGNVAVYQKPKPPGSPKLLYSASYRYSGVPT 60
 |||||||

DB 20 diqmtqspsslasvgdrtvitckasqnvgnvavayqkpkppgspklllysasyrysgvpt 79

QY 61 RFGSGSGTDFTLTISLQEPEDFATYCCOYNIYPLTFGGGTKEIK 107
 |||||||

DB 80 rfgsgsgtdftltisslqepediatyccqynsyprafggtkveik 126

Search completed: January 4, 2002, 18:09:10
 Job time: 275 sec

This Page Blank (uspto)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:05:25 ; Search time 19.66 Seconds
(without alignments)
122.475 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559

Sequence: 1 DIQMTSPSPSLASVGDRTV.....COQNNIYPLTEGQTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/iaa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	92.7	126	4	US-08-646-265A-65
2	514	91.9	126	4	US-08-646-265A-43
3	511	91.4	126	4	US-08-646-265A-47
4	510	91.2	126	4	US-08-646-265A-51
5	509	91.1	126	4	US-08-646-265A-57
6	509	91.1	126	4	US-08-646-265A-63
7	507	90.7	126	4	US-08-646-265A-130
8	507	90.7	126	4	US-08-646-265A-53
9	507	90.7	126	4	US-08-646-265A-85
10	507	90.7	126	4	US-08-646-265A-91
11	507	90.7	126	4	US-08-646-265A-109
12	505	90.3	126	4	US-08-646-265A-59
13	503	90.0	126	4	US-08-646-265A-75
14	502.5	89.9	109	2	US-08-602-725-30
15	500	89.4	107	4	US-08-646-265A-131
16	500	89.4	126	4	US-08-646-265A-87
17	495	88.6	126	4	US-08-646-265A-69
18	495	88.6	126	4	US-08-646-265A-77
19	489	87.5	126	4	US-08-646-265A-73
20	488	86.9	107	2	US-07-934-373C-41
21	486	86.9	107	3	US-08-437-642B-41
22	486	86.9	237	2	US-08-463-587A-25
23	486	86.9	237	2	US-08-463-667A-3
24	486	86.9	237	5	PCT-US91-09133-26
25	486	86.9	126	1	US-08-202-047-13
26	485	86.8	126	1	US-08-202-047-13
27	485	86.8	126	1	US-08-202-047-15

28	485	86.8	126	3	US-08-964-690-13	Sequence 13, Appl
29	485	86.8	126	3	US-08-964-690-15	Sequence 15, Appl
30	482	86.2	109	2	US-07-934-373C-3	Sequence 3, Appl
31	482	86.2	109	3	US-08-437-642B-3	Sequence 3, Appl
32	482	86.2	109	5	PCT-US93-07832-3	Sequence 3, Appl
33	482	86.2	126	4	US-08-646-265A-81	Sequence 81, Appl
34	481	86.0	108	3	US-08-974-899-2	Sequence 2, Appl
35	481	86.0	126	1	US-08-202-047-17	Sequence 17, Appl
36	481	86.0	126	3	US-08-964-690-17	Sequence 17, Appl
37	481	86.0	126	3	US-08-964-690-19	Sequence 19, Appl
38	481	86.0	126	3	US-08-964-690-19	Sequence 19, Appl
39	479	85.7	107	2	US-07-934-373C-18	Sequence 18, Appl
40	479	85.7	107	2	US-07-934-373C-43	Sequence 43, Appl
41	479	85.7	107	3	US-08-437-642B-18	Sequence 18, Appl
42	479	85.7	107	3	US-08-437-642B-43	Sequence 43, Appl
43	479	85.7	107	5	PCT-US93-07832-18	Sequence 18, Appl
44	479	85.7	108	3	US-08-974-899-3	Sequence 3, Appl
45	477	85.3	109	2	US-07-934-373C-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-646-265A-65
; Sequence 65, Application US/08646265A
; Patent No. 6214973
GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshitiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646, 265A
; FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-265A-65

Query Match 92.7%; Score 518; DB 4; Length 126;
Best Local Similarity 93.5%; Pred. No. 5.3e-41;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVVPY 60
DB 20 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVPS 79

OY 61 RFSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
DB 80 RFSGSGCTDFTLTISLQPEDFATYYCOQYNSYPRAFQGTKEIK 126

RESULT 2
US-08-646-265A-43
; Sequence 43, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-43

Query Match 91.9%; Score 514; DB 4; Length 126;
Best Local Similarity 92.5%; Pred. No. 1.2e-40;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVVPY 60
DB 20 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVPS 79

OY 61 RFSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
DB 80 RFSGSGCTDFTLTISLQPEDFATYYCOQYNSYPRAFQGTKEIK 126

DB 80 RFSGSGCTDFTLTISLQPEDFATYYCOQYNSYPRAFQGTKEIK 126

RESULT 3
US-08-646-265A-47
; Sequence 47, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-47

Query Match 91.4%; Score 511; DB 4; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.3e-40;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVVPY 60
DB 20 DIOMTQSSSLASASVGDVTTTCRASQNVGTNAVYQOKPGKAPKLLIYSASFISGVPS 79

OY 61 RFSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
DB 80 RFSGSGCTDFTLTISLQPEDFATYYCOQYNSYPRAFQGTKEIK 126

RESULT 4
US-08-646-265A-51
; Sequence 51, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh

```

? APPLICANT: TSUCHIYA, Masayuki
? TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
? NUMBER OF SEQUENCES: 132
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20007-5109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,265A
? FILING DATE: 09-SEP-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/JP94/01763
? FILING DATE: 19-OCT-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 5-291078
? FILING DATE: 19-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: WEGNER, Harold C.
? REGISTRATION NUMBER: 25,258
? REFERENCE/DOCKET NUMBER: 53466/184
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)672-5300
? TELEFAX: (202)672-5399
? TELEX: 904136
? INFORMATION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 126 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-646-265A-51

Query Match          91.2%; Score 510; DB 4; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.9e-40;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCKASQNVGTNVAWYOQKPKAKLLIYSASFLYSGVPY 60
    |||||||
DB 20 DIQMTSPSSLSASVGRVTITCKASQNVGTNVAWYOQKPKAKLLIYSASFLYSGVPS 79
    |||||||

QY 61 RFGSGSGTDFTLTISLSQPEDFATYYCQOYNIYPLTFGGCTKVEIK 107
    |||||||
DB 80 RFGSGSGTDFTLTISLSQPEDFATYYCQOYNSYPRAFGGCTKVEIK 126
    |||||||

RESULT 5
US-08-646-265A-57
? Sequence 57, Application US/08646265A
? Patent No. 6214973
? GENERAL INFORMATION:
? APPLICANT: OHTOMO, Toshihiko
? APPLICANT: SATO, Koh
? APPLICANT: TSUCHIYA, Masayuki
? TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
? NUMBER OF SEQUENCES: 132
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
```

```

? ZIP: 20007-5109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,265A
? FILING DATE: 09-SEP-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/JP94/01763
? FILING DATE: 19-OCT-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 5-291078
? FILING DATE: 19-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: WEGNER, Harold C.
? REGISTRATION NUMBER: 25,258
? REFERENCE/DOCKET NUMBER: 53466/184
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)672-5300
? TELEFAX: (202)672-5399
? TELEX: 904136
? INFORMATION FOR SEQ ID NO: 57:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 126 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-646-265A-57

Query Match          91.1%; Score 509; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 3.5e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTITCKASQNVGTNVAWYOQKPKAKLLIYSASFLYSGVPY 60
    |||||||
DB 20 DIQMTSPSSLSASVGRVTITCKASQNVGTNVAWYOQKPKAKLLIYSASFLYSGVPS 79
    |||||||

QY 61 RFGSGSGTDFTLTISLSQPEDFATYYCQOYNIYPLTFGGCTKVEIK 107
    |||||||
DB 80 RFGSGSGTDFTLTISLSQPEDFATYYCQOYNSYPRAFGGCTKVEIK 126
    |||||||

RESULT 6
US-08-646-265A-63
? Sequence 63, Application US/08646265A
? Patent No. 6214973
? GENERAL INFORMATION:
? APPLICANT: OHTOMO, Toshihiko
? APPLICANT: SATO, Koh
? APPLICANT: TSUCHIYA, Masayuki
? TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
? NUMBER OF SEQUENCES: 132
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20007-5109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,265A
? FILING DATE: 09-SEP-1996
? CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-63

Query Match 91.1%; Score 509; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 3,5e-40;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVTTTCASQNVGNVAMYQOKPGKAPKLLIYSASFYSGVPY 60
|||||
DB 20 DIOMTQSPSSLSASVGDVTTTCASQNVGNVAMYQOKPGKAPKLLIYSASYRSGVPS 79

OY 61 RFSGSGSGDTFTLTSSLPEDFATYYCOQYNIYPLTFGOGTKVEIK 107
|||||
DB 80 RFSGSGSGDTFTLTSSLPEDFATYYCOQYNIYPLTFGOGTKVEIK 126

RESULT 7
US-08-646-265A-130
Sequence 130, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-130

Query Match 90.7%; Score 507; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 4.6e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVTTTCASQNVGNVAMYQOKPGKAPKLLIYSASFYSGVPY 60
|||||
DB 1 DIOMTQSPSSLSASVGDVTTTCASQNVGNVAMYQOKPGKAPKLLIYSASYRSGVPS 60

OY 61 RFSGSGSGDTFTLTSSLPEDFATYYCOQYNIYPLTFGOGTKVEIK 107
|||||
DB 61 RFSGSGSGDTFTLTSSLPEDFATYYCOQYNIYPLTFGOGTKVEIK 107

RESULT 8
US-08-646-265A-53
Sequence 53, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-646-265A-53

Query Match 90.7%; Score 507; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 5.4e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASFYSGVPY 60
|||||
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPLTFGGGTVEIK 107
|||||
DB 80 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPRAFGGGTVEIK 126

RESULT 9

US-08-646-265A-85
; Sequence 85, Application US/08646265A
; Patent No. 6214973

; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-85

Query Match 90.7%; Score 507; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 5.4e-40;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASFYSGVPY 60
|||||
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPLTFGGGTVEIK 107
|||||
DB 80 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPRAFGGGTVEIK 126

RESULT 10

US-08-646-265A-91
; Sequence 91, Application US/08646265A
; Patent No. 6214973

; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-91

Query Match 90.7%; Score 507; DB 4; Length 126;
Best Local Similarity 91.6%; Pred. No. 5.4e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASFYSGVPY 60
|||||
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPLTFGGGTVEIK 107
|||||
DB 80 RFSGSGSGTDFTLTISLQPEDFATYCCOQYNIYPRAFGGGTVEIK 126

RESULT 11

US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973

```

: GENERAL INFORMATION:
: APPLICANT: OHTOMO, Toshihiko
: APPLICANT: SATO, Koh
: APPLICANT: TSUCHIYA, Masayuki
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
: NUMBER OF SEQUENCES: 132
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: City: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,265A
: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: NO PCT/JP94/01763
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-291078
: FILING DATE: 19-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
: REFERENCE/DOCKET NUMBER: 53466/184
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 109:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 269 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-646-265A-109

Query Match          90.7%; Score 507; DB 4; Length 269;
Best Local Similarity 91.6%; Pred. No. 1,2e-39;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTTCKASQNVGTNVAMYOQPKAKPLIYSASFYSGVPY 60
: |||||||
DB 155 DIOMTQSPSSLSASVGDRTTCKASQNVGTNVAMYOQPKAKPLIYSASFYSGVPS 214
: |||||||

OY 61 RFSSGSGTDFTLTISSLOPEDFATYCCQYNYPLTFGQGTKEIK 107
: |||||||
DB 215 RFSSGSGTDFTLTISSLOPEDFATYCCQYNYSPRAFGQGTKEIK 261
: |||||||

RESULT 12
: US-08-646-265A-59
: Sequence 59, Application US/08646265A
: Patent No. 6214973
: GENERAL INFORMATION:
: APPLICANT: OHTOMO, Toshihiko
: APPLICANT: SATO, Koh
: APPLICANT: TSUCHIYA, Masayuki
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
: NUMBER OF SEQUENCES: 132
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: City: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
```

```

: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,265A
: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: NO PCT/JP94/01763
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-291078
: FILING DATE: 19-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
: REFERENCE/DOCKET NUMBER: 53466/184
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 59:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-646-265A-59

Query Match          90.3%; Score 505; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 8,3e-40;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTTCKASQNVGTNVAMYOQPKAKPLIYSASFYSGVPY 60
: |||||||
DB 20 DIOMTQSPSSLSASVGDRTTCKASQNVGTNVAMYOQPKAKPLIYSASFYSGVPS 79
: |||||||

OY 61 RFSSGSGTDFTLTISSLOPEDFATYCCQYNYPLTFGQGTKEIK 107
: |||||||
DB 80 RFSSGSGTDFTLTISSLOPEDFATYCCQYNYSPRAFGQGTKEIK 126
: |||||||

RESULT 13
: US-08-646-265A-75
: Sequence 75, Application US/08646265A
: Patent No. 6214973
: GENERAL INFORMATION:
: APPLICANT: OHTOMO, Toshihiko
: APPLICANT: SATO, Koh
: APPLICANT: TSUCHIYA, Masayuki
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
: NUMBER OF SEQUENCES: 132
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: City: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
```



```

APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-75

```

```

Query Match          90.0%; Score 503; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-39;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 DIOMTQSPSSLSASVGRVTITCKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPY 60
    |||||||
DB 20 DIOMTQSPSSLSASVGRVSVTCKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPS 79
    |||||||
QY 61 RFGSGSGDTFTLTSSLPEDFAITYCCQYNYITPLTFGGGTVEIK 107
    |||||||
DB 80 RFGSGSGDTFTLTSSLPEDIAIDYFCQYNSYRAFGGTVEIK 126
    |||||||

```

```

RESULT 14
US-08-602-725-30
Sequence 30, Application US/08602725
Patent No. 5965710
GENERAL INFORMATION:
APPLICANT: BODMER, WALTER F.
APPLICANT: DORBIN, HELGA
APPLICANT: SNARY, DAVID
APPLICANT: STEWART, LORNA MD
APPLICANT: YOUNG, SUSAN
APPLICANT: BATES, PAUL A.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 1090-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Humanised kappa light chain
US-08-602-725-30

```

```

Query Match          89.9%; Score 502.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 1.2e-39;
Matches 99; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

```

```

QY 1 DIOMTQSPSSLSASVGRVTITCKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPY 60
    |||||||
DB 1 DIOMTQSPSSLSASVGRVITCKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPS 60
    |||||||
QY 61 RFGSGSGDTFTLTSSLPEDFAITYCCQYNYITPLTFGGGTVEIK 107
    |||||||
DB 61 RFGSGSGDTFTLTSSLPEDIAIDYFCQYNYITPLTFGGGTVEIK 108
    |||||||

```

```

RESULT 15
US-08-646-265A-131
Sequence 131, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184

```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 131:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-265A-131

Query Match 89.4%; Score 500; DB 4; Length 107;
 Best Local Similarity 89.7%; Pred. No. 2e-39;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDVTTTCKASQNVGNVAMWYQOKPGKAPKLLYSASFLYSGVPY 60
 Db 1 DIOMTQSPSSLSASVGDVTTTCKASQNVGNVAMWYQOKPGKAPKLLYSASFLYSGVPS 60
 QY 61 RFSGSGSGTDFTLTITSSLPEDFATYVCOQYNIYPLTFGCGTKVEIK 107
 Db 61 RFSGSGSGTDFTLTITSSLPEDFATYVCOQYNIYPLTFGCGTKVEIK 107

Search completed: January 4, 2002, 18:09:37
 Job time: 252 sec

RESULT 7
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malnqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MID:93178448
A:Accession: S36264
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:218845; NID:933426; PIDD:CAA79297.1; PID:9939919
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-90/Domain: Immunoglobulin homology <IMM>

Query Match 82.1%; Score 459; DB 2; Length 107;
Best Local Similarity 82.2%; Pred. No. 4.2e-33;
Matches 88; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPGKAPKLLIYSASFYSGVPY 60
DB 1 EIVLTQSPSSLSASVGDRTVITCRASQISISYLNWYQKPGKAPKLLIYAASLSQGVPS 60
QY 61 RFSGSGGTDFLTITSLQPEDFAFYTCQYNYPLTFGGGTKEIK 107
DB 61 RFSGSGGTDFLTITSLQPEDFAFYTCQYNYPLTFGGGTKEIK 107

RESULT 8
KIHUBN
Ig kappa chain V-I region (Ban) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 15-Aug-1997
C:Accession: A01878
R:Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.
Mol. Immunol. 23, 73-78, 1986
A:Title: Polymorphism in a kappa I primary (AI) amyloid protein (BAN).
A:Reference number: A01878; MID:86174817
A:Accession: A01878
A:Molecule type: protein
A:Residues: 1-108 <DMO>
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: amyloid; heterotetramer; Immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: Immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
F:23-88/Disulfide bonds: #status predicted

Query Match 82.1%; Score 459; DB 1; Length 108;
Best Local Similarity 83.2%; Pred. No. 4.2e-33;
Matches 89; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPGKAPKLLIYSASFYSGVPY 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQSYNYVAMFQKPGKAPKLLIYDASTLSQGVPS 60

QY 61 RFSGSGGTDFLTITSLQPEDFAFYTCQYNYPLTFGGGTKEIK 107
DB 61 NTFSGSGGTDFLTITSLQPEDFAFYTCQYNSYPTTFGGGTKEIK 107

RESULT 9
S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MID:94060891
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72463
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:30-104/Domain: Immunoglobulin homology <IMM>

Query Match 81.9%; Score 458; DB 2; Length 125;
Best Local Similarity 81.3%; Pred. No. 5.9e-33;
Matches 87; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPGKAPKLLIYSASFYSGVPY 60
DB 15 DIQMTQSPSSLSASVGDRTVITCRASQISISYLNWYQKPGKAPKLLIYAASFSQGVPS 74
QY 61 RFSGSGGTDFLTITSLQPEDFAFYTCQYNYPLTFGGGTKEIK 107
DB 75 RFSGSGGTDFLTITSLQPEDFAFYTCQYNSYPLTFGGGTKEIK 121

RESULT 10
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MID:94080891
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:9441350; PIDD:CAA51109.1; PID:9441351
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:32-106/Domain: Immunoglobulin homology <IMM>

Query Match 81.8%; Score 457; DB 2; Length 123;
Best Local Similarity 84.1%; Pred. No. 7.1e-33;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPGKAPKLLIYSASFYSGVPY 60
DB 17 DIQMTQSPSSLSASVGDRTVITCRASQISISYLNWYQKPGKAPKLLIYAASLSQGVPS 76
QY 61 RFSGSGGTDFLTITSLQPEDFAFYTCQYNYPLTFGGGTKEIK 107
DB 77 RFSGSGGTDFLTITSLQPEDFAFYTCQYNSYPTTFGGGTKEIK 123

RESULT 11
B49047

Ig kappa chain V region (monoclonal strictional autoantibody StrAB SA-1a) - human (fragm
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 456; DB 2; Length 108;
Best Local Similarity 84.1%; Pred. No. 7.7e-33;
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFLYSGVPY 60
|||||
Db 1 DIOMTQSPSSLSASVGDVVTITCKASQSSISLNMVYQOKPGKAPKLLIYAASSLQSGVPS 60
|||||

Oy 61 RFGSGSGTDFLTITSSIQPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||
Db 61 RFGSGSGTDFLTITSSIQPEDFATYYCOQSYSTPLTFGGGTKEIK 107
|||||

RESULT 12
S46376
Ig kappa chain V-J region (733-14) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46376; S36649
R:Benjamin, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; MUID:94313975
A:Accession: S46376
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z21717; NID:9415969; PTDN:CA61701.1; PID:9415970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-99/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 455; DB 2; Length 117;
Best Local Similarity 81.3%; Pred. No. 1e-32;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFLYSGVPY 60
|||||
Db 10 DIOMTQSPSSLSASVGDVVTITCKASQSSISLNMVYQOKPGKAPKLLIYAASSLQSGVPL 69
|||||

Oy 61 RFGSGSGTDFLTITSSIQPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||
Db 70 RFGSGSGTDFLTITSSIQPEDFATYYCOQANSFRTGFGGTKEIK 116
|||||

RESULT 13
S40352
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40352
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891

A:Accession: S40352
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72462; NID:9441392; PTDN:CA51130.1; PID:9441393
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 455; DB 2; Length 131;
Best Local Similarity 82.2%; Pred. No. 1.1e-32;
Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFLYSGVPY 60
|||||
Db 21 DIOMTQSPSSLSASVGNVTITCKASQGISNVLAMVYQOKPGKAPKLLIYAASSLQSGVPS 80
|||||

Oy 61 RFGSGSGTDFLTITSSIQPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||
Db 81 RFGSGSGTDFLTITSSIQPEDFATYYCOQYNSVPTFGGTKEIK 127
|||||

RESULT 14
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40334
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 455; DB 2; Length 132;
Best Local Similarity 80.4%; Pred. No. 1.1e-32;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFLYSGVPY 60
|||||
Db 22 DIOMTQSPSSLSASVGDVVTITCKASQGISNVLAMVYQOKPGKAPKLLIYAASSLQSGVPS 81
|||||

Oy 61 RFGSGSGTDFLTITSSIQPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||
Db 82 RFGSGSGTDFLTITSSIQPEDFATYYCOQFNSVPTFGGTKEIK 128
|||||

RESULT 15
S40336
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40336
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40336
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-124 <KLE>
A:Cross-references: EMBL:X72446; NID:9441360; PTDN:CA51114.1; PID:9441361
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:41 ; Search time 15.29 Seconds

(Without alignments)
256.582 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQVNIYPLTFGGTRKVEIK 107

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459	82.1	108	1	KVIH_HUMAN
2	451	80.7	108	1	KVIH_HUMAN
3	447	80.0	108	1	KVIM_HUMAN
4	445	79.6	108	1	KVIF_HUMAN
5	444	79.4	108	1	KVIG_HUMAN
6	444	79.4	108	1	KVIR_HUMAN
7	440.5	78.8	107	1	KVID_HUMAN
8	440	78.7	108	1	KVIB_HUMAN
9	439	78.5	108	1	KVIB_HUMAN
10	437	78.2	108	1	KVIL_HUMAN
11	434	77.6	108	1	KVIP_HUMAN
12	432	77.3	108	1	KVIS_HUMAN
13	430	76.9	108	1	KVIO_HUMAN
14	428	76.6	108	1	KVIO_HUMAN
15	428	76.6	129	1	KVIW_HUMAN
16	424	75.8	108	1	KVIR_HUMAN
17	422	75.5	108	1	KVIC_HUMAN
18	421	75.3	108	1	KVIA_HUMAN
19	420	75.1	108	1	KVIN_HUMAN
20	417	74.6	108	1	KVIE_HUMAN
21	414	74.1	117	1	KVIL_HUMAN
22	413	73.9	117	1	KVIL_HUMAN
23	407	72.8	129	1	KVIX_HUMAN
24	403	72.1	149	1	KVSA_MOUSE
25	392.5	70.2	109	1	KVIT_HUMAN
26	392	70.1	112	1	KVIO_HUMAN
27	391	69.9	108	1	KVSI_MOUSE
28	390.5	69.9	129	1	KVSH_HUMAN
29	389.5	69.7	129	1	KVSI_HUMAN
30	387	69.2	108	1	KV50_MOUSE
31	386	69.1	108	1	KV5T_MOUSE
32	384	68.7	108	1	KV5S_MOUSE
33	383.5	68.6	109	1	KV3D_HUMAN

34	382.5	68.4	129	1	KV3M_HUMAN
35	382	68.3	108	1	KV5D_MOUSE
36	381	68.2	134	1	KV4C_HUMAN
37	380.5	68.1	109	1	KV3B_HUMAN
38	380	68.0	128	1	KV5E_MOUSE
39	378.5	67.7	109	1	KV3F_HUMAN
40	378	67.6	108	1	KV5P_MOUSE
41	377	67.4	114	1	KV4A_HUMAN
42	377	67.4	136	1	KV5B_MOUSE
43	376	67.3	108	1	KV5L_MOUSE
44	376	67.3	108	1	KV5R_MOUSE
45	375.5	67.2	109	1	KV3E_HUMAN

ALIGNMENTS

RESULT	1	STANDARD	PRT	108 AA.
KVIH_HUMAN				
ID	KVIH_HUMAN			
AC	P04430			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-I REGION BAN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=86174817; PubMed=3083240;			
RA	Dwulet F.E., O'Connor T.P., Benson M.D.;			
RT	"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";			
RL	Mol. Immunol. 23:73-78(1986).			
DR	PIR: A01878; KIHUBN.			
DR	HSSP: P80362; IWTI.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART: SM00406; IgV; 1.			
KW	Immunoglobulin V region; Amyloid.			
FT	DOMAIN 1 23 FRAMEWORK 1.			
FT	DOMAIN 2 34 FRAMEWORK 2.			
FT	DOMAIN 3 56 FRAMEWORK 3.			
FT	DOMAIN 4 89 FRAMEWORK 4.			
FT	DOMAIN 5 97 COMPLEMENTARITY-DETERMINING 3.			
FT	DOMAIN 6 107 COMPLEMENTARITY-DETERMINING 4.			
FT	DISULFID 23 88 BY SIMILARITY.			
FT	NON_TER 108 108			
SQ	SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;			
Query Match	82.1%; Score 459; DB 1; Length 108;			
Best Local Similarity	83.2%; Pred. No. 1,1e-41;			
Matches	89; Conservative 6; Mismatches 12; Indels 0; Gaps 0;			
OY	1 DIQMTQSPSSLSASVGRVTITCKASQNVGTVAMVYQDQPKAPKRLIYSASFYSGVY 60			
DB	1 DIQMTQSPSSLSASVGRVITTCRASQSVYVAMFQDQPKAPKRLIYDASTLQSGVPS 60			
OY	61 RFSSGSGTDFTLTITSLQPEDFATYYCQYNIYPLTFGGGTKVEIK 107			
DB	61 NETSSGSDTDLITLTSLQPEDFATYYCQYNSPYTFGGGTKVQIK 107			
RESULT	2			
ID	KVIH_HUMAN	STANDARD:	PRT:	108 AA.
AC	P01600;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Matanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01868; KIHUHU.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 98 107 FRAMEWORK 4.
FT NON_TER 23 88 BY SIMILARITY.
FT SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.7%; Score 451; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 7.8e-41;
Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGVDRVTITCKASQNVGVNANYQOKPGKAPRLIYASFLYSGVPY 60
DB 1 DIQMTPSSLSASVGVDRVTITCKASQNVGVNANYQOKPGKAPRLIYASFLYSGVPY 60
QY 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107

RESULT 3
KVIM_HUMAN STANDARD; PRT; 108 AA.
ID KVIM_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
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DR PIR: A01871; KIHULY.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 98 107 FRAMEWORK 4.
FT NON_TER 23 88 BY SIMILARITY.
FT SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 80.0%; Score 447; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 2.1e-40;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGVDRVTITCKASQNVGVNANYQOKPGKAPRLIYASFLYSGVPY 60
DB 1 DIQMTPSSLSASVGVDRVTITCKASQNVGVNANYQOKPGKAPRLIYASFLYSGVPY 60
QY 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107

RESULT 4
KVIF_HUMAN STANDARD; PRT; 108 AA.
ID KVIF_HUMAN
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION EU.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RT Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RT Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR: A01866; KIHUHU.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
```


RT protein.";
 RL Eur. J. Biochem. 49:377-391(1974).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR: A01864; KIHUAD.
 DR HSP: P80362; IHWL.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003596; Iq_V.
 DR Pfam: PF00047; Iq; 1.
 DR SMART: SM00406; Iq; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOXYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C346 CRC64;
 Query Match 78.8%; Score 440.5; DB 1; Length 107;
 Best Local Similarity 78.5%; Pred. No. 9.8e-40;
 Matches 84; Conservative 12; Mismatches 10; Indels 1; Gaps 1;
 Oy 1 DIQMTSPSSLSASVGDVITTCASQNVGTNAVWYQOKPKAPRLIYASFLYSGVPY 60
 Db 1 DIQMTSPSSLSASVGDVITTCASQNVGTNAVWYQOKPKAPRLIYASFLYSGVPY 60
 Oy 61 RFSSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGGCTKVEIK 107
 Db 61 RFSSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGGCTKVEIK 107
 RESULT 8
 KVIY_HUMAN STANDARD; PRT; 108 AA.
 ID KVIY_HUMAN
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE. AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95086080; PubMed=793911;
 RA Huang D.-B., Chang C.-H., Almsworth C., Bruenger A.T., Eultz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural origin of altered domain interactions in immunoglobulin
 RT light-chain dimers";
 RL Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE=81267384; PubMed=6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Wat.";
 RL J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PDB: 1MTL; 01-NOV-94.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003596; Iq_V.
 DR Pfam: PF00047; Iq; 1.
 DR SMART: SM00406; Iq; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 FRAMEWORK 2.
 FT DOMAIN 3 49 FRAMEWORK 3.
 FT DOMAIN 4 56 FRAMEWORK 4.
 FT DOMAIN 5 57 FRAMEWORK 5.
 FT DOMAIN 6 88 FRAMEWORK 6.
 FT DOMAIN 7 89 FRAMEWORK 7.
 FT DOMAIN 8 97 FRAMEWORK 8.
 FT DOMAIN 9 107 FRAMEWORK 9.
 FT DOMAIN 10 107 FRAMEWORK 10.

FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
 Query Match 78.7%; Score 440; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 1.1e-39;
 Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 Oy 1 DIQMTSPSSLSASVGDVITTCASQNVGTNAVWYQOKPKAPRLIYASFLYSGVPY 60
 Db 1 DIQMTSPSSLSASVGDVITTCASQNVGTNAVWYQOKPKAPRLIYASFLYSGVPY 60
 Oy 61 RFSSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGGCTKVEIK 107
 Db 61 RFSSGSGCTDFTLTISLQPEDFATYYCOQYNIYPLTFGGCTKVEIK 107
 RESULT 9
 KVIY_HUMAN STANDARD; PRT; 108 AA.
 ID KVIY_HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN RET.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A01862; KIHUAD.
 DR HSP: P01607; IREI.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003596; Iq_V.
 DR Pfam: PF00047; Iq; 1.
 DR SMART: SM00406; Iq; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 2 34 FRAMEWORK 2.
 FT DOMAIN 3 49 FRAMEWORK 3.
 FT DOMAIN 4 56 FRAMEWORK 4.
 FT DOMAIN 5 57 FRAMEWORK 5.
 FT DOMAIN 6 88 FRAMEWORK 6.
 FT DOMAIN 7 89 FRAMEWORK 7.
 FT DOMAIN 8 97 FRAMEWORK 8.
 FT DOMAIN 9 107 FRAMEWORK 9.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;
 Query Match 78.5%; Score 439; DB 1; Length 108;
 Best Local Similarity 80.4%; Pred. No. 1.4e-39;

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=68362076; PubMed=5595110;
RX Hilschmann N.;
RA "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.).
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01874; KIHURY.
DR HSR: P80362; IWTU.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 7 97 FRAMEWORK 4.
FT DOMAIN 8 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 77.6%; Score 434; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. NO. 4.8e-39;
Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTPSSISASVGDREVITTCRKSQWGTNVAYQQRPKAPRLTIYSASFYSGVPY 60
Db 1 DIQMTPSSISASVGDREVITTCRKSQWGTNVAYQQRPKAPRLTIYSASFYSGVPY 60
QY 61 RPSGSGSTDEFTLTISLQPEDFATRYQQQYNYPLRFEGQTKYEIK 107
Db 61 RPSGSGSTDEFTLTISLQPEDFATRYQQQYNYPLRFEGQTKYEIK 107

RESULT 12
KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wess).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

```

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01877; KIHUWS.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 57 FRAMEWORK 3.
FT DOMAIN 7 88 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SO SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 77.3%; Score 432; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 7.8e-39;
Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
OY 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNAVYQOKPKAPRLIYSASFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNAVYQOKPKAPRLIYSASFLYSGVPY 60
OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNNIYPLTFGGTKVEIK 107
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNNIYPLTFGGTKVEIK 107

RESULT 13
KV10_HUMAN STANDARD: PRT: 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION SCW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides and the complete amino acid sequence.";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01875; KIHUSW.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 57 FRAMEWORK 3.
FT DOMAIN 7 88 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108

SO SEQUENCE 108 AA; 11764 MW; 32CEDDDF9644414 CRC64;

Query Match 76.9%; Score 430; DB 1; Length 108;
Best Local Similarity 76.6%; Pred. No. 1.3e-38;
Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

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DB 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNAVYQOKPKAPRLIYSASFLYSGVPY 60
OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNNIYPLTFGGTKVEIK 107
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNNIYPLTFGGTKVEIK 107

RESULT 14
KV10_HUMAN STANDARD: PRT: 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION REI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); Isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01873; KIHURE.
DR PDB: IREI; 17-FEB-84.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 57 FRAMEWORK 3.
FT DOMAIN 7 88 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT STRAND 30 31
FT TURN 33 38
FT STRAND 40 41
FT TURN 45 49
FT TURN 50 52

FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11922 MW; 9E8143E1188BCE2A CRC64;

Query Match 76.6%; Score 428; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 2.1e-38;
 Matches 83; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60
 DB 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60
 QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYNIYPLTFGGCTKVEI 106
 DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYNIYPLTFGGCTKVEI 106

RESULT 15

KV1W_HUMAN STANDARD; PRT; 129 AA.

AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-85014148; PubMed-6091049;
 RA Klobbeck H.G., Combrato G., Zachau H.G.;
 RT "Immunoglobulin genes of the kappa light chain type from two human
 lymphoid cell lines are closely related";
 RL Nucleic Acids Res. 12:6995-7006(1984).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: X00965; CAA25477.1; ALT_TERM.

DR PIR: A01883; KIHUK.
 DR HSSP: P01607; IRET.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45
 FT DOMAIN 46 56
 FT DOMAIN 57 71
 FT DOMAIN 72 78
 FT DOMAIN 79 110
 FT DOMAIN 111 119
 FT DOMAIN 120 129
 FT DISULFID 45 110
 IG KAPPA CHAIN V-I REGION WALKER.
 FRAMEWORK 1.
 COMPLEMENTARITY-DETERMINING 1.
 FRAMEWORK 2.
 COMPLEMENTARITY-DETERMINING 2.
 FRAMEWORK 3.
 COMPLEMENTARITY-DETERMINING 3.
 FRAMEWORK 4.
 BY SIMILARITY.

FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match 76.6%; Score 428; DB 1; Length 129;
 Best Local Similarity 79.4%; Pred. No. 2.5e-38;
 Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60
 DB 23 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 82
 QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCQOYNIYPLTFGGCTKVEI 107
 DB 83 RFGSGSGTDFLTITSSLOPEDFATYYCQOYNIYPLTFGGCTKVEI 129

Search completed: January 4, 2002, 18:14:37
 Job time: 296 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:08:31 ; Search time 37.65 Seconds
(without alignments)
415.701 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559

Sequence: 1 DIOMTQSPSSLSASVGDVRT.....COQYNLYPLTFGGTKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues 473505

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	80.1	108	4 Q9UL70	Q9UL70 homo sapien
2	441	78.9	108	4 Q9UL77	Q9UL77 homo sapien
3	432	77.3	108	4 Q9UL79	Q9UL79 homo sapien
4	420.5	75.2	107	4 Q9UL81	Q9UL81 homo sapien
5	399	71.4	108	4 Q9UL83	Q9UL83 homo sapien
6	392.5	70.2	109	4 Q9UL85	Q9UL85 homo sapien
7	384	68.7	214	11 Q9LIAS	Q9LIAS mus musculu
8	379.5	67.9	109	4 Q9UL78	Q9UL78 homo sapien
9	374	66.9	298	11 Q9OYF0	Q9OYF0 mus musculu
10	372	66.5	107	11 Q9UL84	Q9UL84 mus musculu
11	353.5	63.2	109	4 Q9UL86	Q9UL86 homo sapien
12	343	61.4	99	11 Q9UL74	Q9UL74 mus musculu
13	342.5	61.3	106	5 Q9UL10	Q9UL10 schistosoma
14	334	59.7	107	11 Q9ER29	Q9ER29 mus musculu
15	325.5	58.2	238	11 Q9NM37	Q9NM37 mus musculu
16	306	54.7	101	11 Q9UL78	Q9UL78 mus musculu
17	305	54.6	103	11 Q9JL80	Q9JL80 mus musculu
18	298	53.3	97	11 Q9JL76	Q9JL76 mus musculu
19	294	52.6	109	6 Q9N0W5	Q9N0W5 oryctolagus

20	292.5	52.3	104	11 Q9UL82	Q9UL82 mus musculu
21	288	51.5	114	4 Q9UL80	Q9UL80 homo sapien
22	214	38.3	107	4 Q9UL82	Q9UL82 homo sapien
23	208.5	37.3	107	4 Q9NSD6	Q9NSD6 mus musculu
24	196.5	35.2	235	11 Q9NM11	Q9NM11 mus musculu
25	178	31.8	130	4 Q9NP29	Q9NP29 mus musculu
26	154.5	27.6	109	11 Q9ET13	Q9ET13 mus musculu
27	151.5	27.1	334	13 Q9IB05	Q9IB05 spherooides
28	149.5	26.7	337	13 Q9IB02	Q9IB02 spherooides
29	143	25.6	93	4 Q9UL76	Q9UL76 mus musculu
30	142	25.4	135	4 Q9HS24	Q9HS24 mus musculu
31	135.5	24.2	484	11 Q99LA6	Q99LA6 mus musculu
32	134	24.0	342	13 Q9IB00	Q9IB00 spherooides
33	130	23.3	123	11 Q61243	Q61243 mus musculu
34	121.5	21.7	337	13 Q9IA24	Q9IA24 spherooides
35	120	21.5	320	13 Q9IA29	Q9IA29 spherooides
36	118.5	21.2	509	11 Q9QX57	Q9QX57 mus musculu
37	118.5	21.2	513	11 P97797	P97797 mus musculu
38	112.5	20.1	122	4 Q99604	Q99604 mus musculu
39	112.5	20.1	137	4 Q9UDR1	Q9UDR1 mus musculu
40	112.5	20.1	509	11 Q08907	Q08907 mus musculu
41	112	20.0	318	13 Q9IB03	Q9IB03 spherooides
42	111.5	19.9	339	13 Q9IAY8	Q9IAY8 spherooides
43	110.5	19.8	122	4 Q99603	Q99603 mus musculu
44	109.5	19.6	332	13 Q9IB08	Q9IB08 spherooides
45	108	19.3	118	4 Q9UL72	Q9UL72 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	108 AA.
Q9UL70	Q9UL70			
AC	Q9UL70			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.			
CC	EMBL: AF035044; AAD56280.1; -			
DR	HSSP: P01607; IREL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; IgV.1.			
DR	SMART: SM00406; IGV.1.			
FT	NON_TER 1			
FT	NON_TER 108			
SO	SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;			
Query Match	80.1%; Score 448; DB 4; Length 108;			
Best Local Similarity	81.3%; Pred. No. 6,1e-41;			
Matches	87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;			
QY	1 DIOMTQSPSSLSASVGDVRTITCKASQNGFNVAAYQOKGKAPKLLIYSASFLYSGVPY 60			
DB	1 DIOMTQSPSSLSASVGDVRTITCKASQISNLYAWYQOKGKVPKSLIYASTLQSGVPS 60			
QY	61 RFGSGSGVTFITLITSLQPEDFATYYCQQYNLYPLTFGGTKEIK 107			

```
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107
|||||
RESULT 2
ID Q9UL77 PRELIMINARY: PRT: 108 AA.
AC Q9UL77:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 78.9%; Score 441; DB 4; Length 108;
Best Local Similarity 81.3%; Pred. No. 3.5e-40;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Db 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Qy 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNIPYLPFGQGTKEIK 107
|||||
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYVSEPTFGQGTKEIK 107
|||||

RESULT 3
ID Q9UL79 PRELIMINARY: PRT: 108 AA.
AC Q9UL79:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 77.3%; Score 432; DB 4; Length 108;
Best Local Similarity 78.5%; Pred. No. 3.2e-39;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Db 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Qy 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNIPYLPFGQGTKEIK 107
|||||
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYVSEPTFGQGTKEIK 107
|||||

RESULT 4
ID Q9UL81 PRELIMINARY: PRT: 107 AA.
AC Q9UL81:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035033; AAD56269.1; -.
DR HSSP: P80362; IWTI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.2%; Score 420.5; DB 4; Length 107;
Best Local Similarity 78.5%; Pred. No. 5.6e-38;
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Db 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Qy 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNIPYLPFGQGTKEIK 107
|||||
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYVSEPTFGQGTKEIK 107
|||||

RESULT 5
ID Q9UL83 PRELIMINARY: PRT: 108 AA.
AC Q9UL83:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;
```

```
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 77.3%; Score 432; DB 4; Length 108;
Best Local Similarity 78.5%; Pred. No. 3.2e-39;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Db 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Qy 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNIPYLPFGQGTKEIK 107
|||||
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYVSEPTFGQGTKEIK 107
|||||

RESULT 4
ID Q9UL81 PRELIMINARY: PRT: 107 AA.
AC Q9UL81:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035033; AAD56269.1; -.
DR HSSP: P80362; IWTI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.2%; Score 420.5; DB 4; Length 107;
Best Local Similarity 78.5%; Pred. No. 5.6e-38;
Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Db 1 DIQMTQSPSSLSASVGDVTTTCRASQNVGTVMVYQOKPGKAPKLLIYASFLYSGVPY 60
|||||
Qy 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYNIPYLPFGQGTKEIK 107
|||||
Db 61 RFSGSGSTDFLTITSSLOPEDVATYCOQYVSEPTFGQGTKEIK 107
|||||

RESULT 5
ID Q9UL83 PRELIMINARY: PRT: 108 AA.
AC Q9UL83:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
CC EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:10 ; Search time 38.05 Seconds
(without alignments)
25.308 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70
Sequence: 1 SSPYTKSFNRGEC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.1101:*

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- 3: /SID88/gcgdata/geneseq/AA1982.DAT:*
- 4: /SID88/gcgdata/geneseq/AA1983.DAT:*
- 5: /SID88/gcgdata/geneseq/AA1984.DAT:*
- 6: /SID88/gcgdata/geneseq/AA1985.DAT:*
- 7: /SID88/gcgdata/geneseq/AA1986.DAT:*
- 8: /SID88/gcgdata/geneseq/AA1987.DAT:*
- 9: /SID88/gcgdata/geneseq/AA1988.DAT:*
- 10: /SID88/gcgdata/geneseq/AA1989.DAT:*
- 11: /SID88/gcgdata/geneseq/AA1990.DAT:*
- 12: /SID88/gcgdata/geneseq/AA1991.DAT:*
- 13: /SID88/gcgdata/geneseq/AA1992.DAT:*
- 14: /SID88/gcgdata/geneseq/AA1993.DAT:*
- 15: /SID88/gcgdata/geneseq/AA1994.DAT:*
- 16: /SID88/gcgdata/geneseq/AA1995.DAT:*
- 17: /SID88/gcgdata/geneseq/AA1996.DAT:*
- 18: /SID88/gcgdata/geneseq/AA1997.DAT:*
- 19: /SID88/gcgdata/geneseq/AA1998.DAT:*
- 20: /SID88/gcgdata/geneseq/AA1999.DAT:*
- 21: /SID88/gcgdata/geneseq/AA2000.DAT:*
- 22: /SID88/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	106	9 AAP81028	C region of L chain
2	70	100.0	106	14 AAP41687	undefined ORF1 enc
3	70	100.0	106	14 AAP43686	Human kappa consta
4	70	100.0	106	18 AAP37347	Immunoglobulin C-k
5	70	100.0	106	19 AAP59622	Anti-RSV F protein
6	70	100.0	106	19 AAP48649	Constant region of
7	70	100.0	106	22 AAP04072	Interleukin recept
8	70	100.0	107	19 AAP40578	Human kappa CL dom
9	70	100.0	107	20 AAP50152	Human kappa light
10	70	100.0	107	20 AAP08745	Human kappa-CL dom
11	70	100.0	107	20 AAP92425	Human kappa protei

12	70	100.0	107	21 AAP27000	Human kappa CL dom
13	70	100.0	107	22 AAP62265	Light chain constr
14	70	100.0	108	20 AAP70802	Amino acid sequen
15	70	100.0	108	21 AAP92191	Human IgG1 kappa d
16	70	100.0	143	10 AAP93559	Sequence of human
17	70	100.0	143	22 AAG75780	Human colon cancer
18	70	100.0	201	20 AAP29770	P-selectin ligand
19	70	100.0	213	17 AAP04301	Antibody fusion pr
20	70	100.0	213	17 AAP05830	Humanised M291 ant
21	70	100.0	213	22 AAP83157	Ganglioside GM2 an
22	70	100.0	214	14 AAP30776	H5216-158 murine a
23	70	100.0	214	14 AAP43338	Completely humanis
24	70	100.0	214	17 AAP05828	Humanised ID10 ant
25	70	100.0	214	17 AAP00373	Anti-CD18 chimeric
26	70	100.0	214	18 AAP45517	NANUC-2 light chain
27	70	100.0	214	18 AAP34504	Light chain of hum
28	70	100.0	214	18 AAP34506	Light chain of ful
29	70	100.0	214	18 AAP07615	Ulcerative colitis
30	70	100.0	214	19 AAP64671	Human UC PANCA mon
31	70	100.0	214	19 AAP49815	Amino acid sequen
32	70	100.0	214	20 AAP34039	NANUC-2 antibody 1
33	70	100.0	214	20 AAP30202	Light chain sequen
34	70	100.0	214	20 AAP08754	Human antibody huf
35	70	100.0	214	20 AAP08599	Anti-human TNF- α lp
36	70	100.0	214	20 AAP08600	JPL1127855 Seg ID
37	70	100.0	214	20 AAP06842	Seq ID No:10 of JP
38	70	100.0	214	20 AAP95615	Humanized anti-CD1
39	70	100.0	214	20 AAP30632	Recombinant human1
40	70	100.0	214	21 AAP29407	Human monoclonal a
41	70	100.0	214	21 AAP93735	The kappa chain of
42	70	100.0	214	21 AAP57337	UC PANCA Mab NANUC
43	70	100.0	215	22 AAP65777	Rhumab CD18 light
44	70	100.0	215	18 AAP07616	Ulcerative colitis
45	70	100.0	215	19 AAP64673	Human UC PANCA mon

ALIGNMENTS

RESULT 1	
ID AAP81028	standard; protein; 106 AA.
XX	
AC AAP81028:	
XX	
DT 17-OCT-1990	(first entry)
XX	
DE C region of L chain (chi) of human antibody.	
XX	
KW mouse-human chimeric antibody ; anticancer agent;	
KW human common acute lymphocytic leukaemia; ss.	
XX	
OS Homo sapiens.	
XX	
PN EP255694-A.	
XX	
PD 10-FEB-1988.	
XX	
PF 29-JUL-1987:	87EP-0110994.
XX	
PR 30-JUL-1986:	86JP-0177809.
XX	
PA (TEIJ) TEIJIN KK.	
XX	
PI Nishimura Y, Ichikawa Y, Kudo A, Watanabe T;	
XX	
DR WPI; 1988-037653/06.	
XX	
PT Mouse-human chimera antibody -	
PT used for diagnosis and therapy of human common acute lymphocytic	
PT leukaemia	
XX	
PS Disclosure; ; P: English.	

XX The chimeric antibody comprises a C region of human origin linked
CC to a V region of mouse origin in both the L and H chains. The mouse
CC -derived V region is opt. reactive with human common lymphocytic
CC leukaemia antigen.
CC See also AAN81358-9, AAN81360, AAN81362-6 and AAP81025-7.

XX Sequence 106 AA:

Query Match 100.0%; Score 70; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
Db 94 sspvtsfngrec 106
|||||

RESULT 2

AAR41687
ID AAR41687 standard; Protein: 106 AA.

XX AAR41687;

XX 20-OCT-1993 (first entry)

XX Undefined ORF1 encoded by plasmid pAH4611.

DE Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;
KW chain; variable; constant; anti-human; transferrin; receptor;
KW antibody; brain; capillary; endothelial cell; conjugate; epilepsy;
KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke;
KW Parkinsons disease; Alzheimers disease.

XX Synthetic.

XX W09310819-A.

XX 10-JUN-1993.

XX 24-NOV-1992; 92WO-US10206.

XX 26-NOV-1991; 91US-0800458.

XX (ALKE-) ALKERMES INC.

XX Friden PM;

XX WPI: 1993-196742/24.

XX N-PSDB; AAQ43845.

PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders

XX Disclosure; Fig 13H; 151pp; English.

XX The sequences given in AAR41686-87 represent proteins encoded by the
CC expression vector pAH4611. This vector was produced from the plasmid
CC pMG4270. pMG4270 is the expression vector for the light chain
CC variable region (VL) of the antibody 128.1 which was obtained by PCR
CC with leader/J region priming (see also AAQ43842). The vector also
CC contains an ampicillin resistance gene, a gpt (mycophenolic acid
CC resistance) selected marker, an immunoglobulin H enhancer and an
CC intron for V-constant region splicing. Transcription of the CH gene
CC is from the VH promoter of the murine 27.44 gene. The cloning of
CC the 128.1 VL region was accomplished in two stages with the production
CC of plasmid pSV4271 as an intermediate vector which lacks the promoter
CC region. This plasmid was used in conjunction with pAH4602 in the
CC production of the chimeric antibody 128.1. 128.1 is an anti-human
CC transferrin receptor antibody which binds to the transferrin receptor
CC on brain capillary endothelial cells. This antibody may be used in a

CC conjugate in which it is linked to a neuropharmacological or diagnostic
CC agent. The conjugate may be used to treat or prevent neurological
CC disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and
CC Alzheimers disease. It may also be used for diagnostic methods.

XX Sequence 106 AA:

Query Match 100.0%; Score 70; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
Db 94 sspvtsfngrec 106
|||||

RESULT 3

AAR43686
ID AAR43686 standard; Protein: 106 AA.

XX AAR43686;

XX 25-MAY-1994 (first entry)

XX Human kappa constant domain as encoded by pHCW-KR.

DE Human; immunoglobulin; constant; region; humanised; P-selectin; light;
KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;
KW monoclonal; PBL.3; CDR; complementarily determining region; leukocyte;
KW expression vector; coexpression; pHCW-1748RLA-gammaCI-dhfr; epitope;
KW pHCW-1748RLA-KR-neo; PBL.3/humanised version A; vascular endothelium;
KW pHCW-1747CH-gammaCI-neo; pHCW-1747-CL-KR-neo; PBL.3 chimera;
KW acute lung injury; ischaemia reperfusion injury; inflammation.

XX Homo sapiens.

XX W09321956-A.

XX 11-NOV-1993.

XX 04-MAY-1993; 93WO-US04274.

XX 05-MAY-1992; 92US-0880196.

XX (CYTE-) CYTEL CORP.

XX Chestnut RW, Paulson JC, Polley MJ;

XX WPI: 1993-368423/46.

XX N-PSDB; AAQ51548.

PT Anti-P-selectin antibody for ischaemia acute lung injury treatment -
PT useful to treat inflammation and pathological conditions of
PT intercellular adhesion by competitive inhibition assays

XX Example 10; Fig 10; 82pp; English.

XX The sequences given in AAR43685-86 represent human immunoglobulin
CC constant regions which were used in the production of the humanised
CC P-selectin blocking antibody, along with the heavy and light chain
CC variable region coding sequences of the murine monoclonal antibody
CC PBL.3, given in AAR43687-88. The CDRs of human heavy and light
CC chains were substituted for the CDRs of human heavy and light chains.
CC The humanised variable regions were inserted into expression vectors.
CC By coexpression of appropriate combinations of heavy and light
CC chains, several humanised antibodies can be expressed. Coexpression
CC of pHCW-1748RLA-gammaCI-dhfr and pHCW-1748RLA-KR-neo gives rise
CC to the PBL.3/humanised version A. Coexpression of pHCW-1747CH-
CC gammaCI-neo and pHCW-1747-CL-KR-neo gives rise to the PBL.3 chimera.
CC These humanised antibodies selectively bind epitopes on P-selectin and
CC block adhesion of leukocytes to the vascular endothelium. They may be
CC used to treat inflammatory and thrombotic diseases and other

CC pathological conditions involving P-selectin and antibodies to it, esp.
 CC acute lung injury and ischaemia reperfusion injury.

XX Sequence 106 AA;

Query Match 100.0%; Score 70; DB 14; Length 106;

Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNNGEC 13

DB 94 sspvtskfngrec 106

RESULT 4

AAW37347

XX AAW37347 standard; Protein; 106 AA.

XX AAW37347;

XX 11-MAY-1998 (first entry)

XX Immunoglobulin C-kappa region.

XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;

XX gene amplification; immunotherapy; therapy; immunoglobulin;

XX C-kappa; constant region.

XX Homo sapiens.

XX WO9741244-A1.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US07039.

XX 06-DEC-1996; 96US-0761277.

XX 01-MAY-1996; 96US-0644664.

XX (GENI-) GENITOPE CORP.

XX Denney DW;

XX WPI: 1997-549743/50.

XX N-PSDB: AAT97190.

XX Multivalent vaccine to treat B cell lymphoma or leukaemia -

XX comprises at least 2 different recombinant variable regions of

XX immunoglobulin molecules derived from B cell lymphoma cells

XX Example 10; Page 127-128; 177pp; English.

XX This protein comprises an immunoglobulin (Ig) C-kappa region.

XX The invention provides a method for the production of tumour-

XX specific Ig derived from a B-cell lymphoma patient. In the novel

XX method, expression plasmids containing the patient's VH region(s)

XX joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)

XX sequence and expression plasmids containing the patient's VL

XX region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2

XX (see AAT97191) sequence are cotransfected along with a selectable and

XX amplified marker into a cell line (e.g. BW5147.G.1.4), and

XX transfected cells are then subjected to selection and amplification.

XX The method permits the production of a multivalent vaccine which

XX reflects the degree of somatic variation found within the patient's

XX tumour. These novel multivalent vaccines provide superior vaccines

XX for the treatment of B-cell lymphoma.

XX Sequence 106 AA;

XX Query Match 100.0%; Score 70; DB 18; Length 106;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNNGEC 13

DB 94 sspvtskfngrec 106

RESULT 5

AAW59622

XX AAW59622 standard; Protein; 106 AA.

XX AAW59622;

XX 12-OCT-1998 (first entry)

XX Anti-RSV F protein Hu19 MAb light chain constant region.

XX Monoclonal antibody; human; Hu19C; Hu19D; engineered antibody; RSV;

XX respiratory syncytial virus; complementarity determining region;

XX CDR; infection; immunotherapy; therapy; diagnosis.

XX Homo sapiens.

XX WO9819704-A1.

XX 14-MAY-1998.

XX 23-OCT-1997; 97WO-US19203.

XX 01-NOV-1996; 96US-0030149.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Deen KC, Dillon SB, Porter TG, Sweet RW;

XX WPI: 1998-286600/25.

XX Monoclonal antibodies reactive with Respiratory Syncytial Virus -

XX useful for detection, prevention and treatment of RSV infections

XX Disclosure; Fig 3; 109pp; English.

XX This is the amino acid sequence of the light chain constant region

XX (C kappa) of constructs 19C and 19D of novel human monoclonal

XX antibodies (MAbs) reactive with the fusion (F) protein of

XX respiratory syncytial virus (RSV). Hu19A, Hu19B, Hu19C and Hu19D

XX MAbs are claimed. These are reshaped human antibodies comprising a

XX heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18); and

XX a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).

XX Such engineered antibodies are neutralising; they inhibit virus

XX growth in vitro and in vivo in animal models of RSV infection.

XX They can be used in the detection, prevention and passive

XX immunotherapy of RSV infection. Nucleic acids encoding the human

XX MAbs, recombinant plasmids (see AAV1427-33) and host cells (e.g.

XX COS, CHO, myeloma) are provided.

XX Sequence 106 AA;

XX Query Match 100.0%; Score 70; DB 19; Length 106;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNNGEC 13

DB 94 sspvtskfngrec 106

RESULT 6

AAW48649

XX AAW48649 standard; Protein; 106 AA.

XX AAW48649;

```

XX 04-AUG-1998 (first entry)
DT Constant region of hmAb425 light chain.
XX
DE Antibody-cytokine fusion protein: tricistronic vector:
XX TNF alpha; IL-2; IRES; internal ribosome entry site.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9811241-A1.
XX
PD 19-MAR-1998.
XX
PF 02-SEP-1997; 97WO-EP04765.
XX
PR 30-SEP-1996; 96EP-0115635.
PR 16-SEP-1996; 96EP-0114820.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C;
PI Rieke E, Von Hoegen I, Welge T;
XX
DR WPI: 1998-207400/18.
DR N-PSDB: AAV18096.
XX
PT Oligo:cistronic expression vector - useful for production of, e.g.
PT MAb425/TNF- $\alpha$  or MAb425/IL-2 antibody fusion protein
XX
PS Disclosure: Fig 15; 89pp; English.
XX
CC The present sequence represents the constant region of the humanized
CC monoclonal antibody 425 (hmAb425) light chain. The hmAb425 has
CC specificity for the human EGF receptor. The invention claims for a
CC new pmcIdMAP tricistronic vector (AAV18096) for the expression of an
CC antibody-cytokine fusion protein, hmAb425-TNF alpha. hmAb425-TNF
CC alpha comprises of the TNF alpha, fused to the C-terminus of the heavy
CC chain of the hmAb425. The TNF alpha sequence can be substituted by the
CC IL-2 sequence. The vector also contains a strong promoter/enhancer
CC unit, a selection marker gene and at least two poliovirus derived
CC internal ribosomal entry site (IRES) sequences. The vector can be
CC expressed in mammalian host cells for the production of heteromeric
CC fusion proteins. This expression system is claimed to produce the
CC heteromeric proteins in high yields.
CC
XX Sequence 106 AA:
SQ

```

Query Match 100.0%; Score 70; DB 19; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 SSPVTKSFNRGEC 13
Db 94 sspvtksfnrgec 106

```

RESULT 7
 AAB04072
 ID AAB04072 standard; Protein: 106 AA.
 AC AAB04072;
 XX
 DT 11-APR-2001 (first entry)
 XX
 DE Interleukin receptor subunit::human kappa light chain fusion protein.
 XX
 KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
 KW binding; detection; modulation; recombinant cell;
 KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;
 KW immune system; blood; bone; inflammatory response; inflammation;

```

KW spleen; human.
XX
XX Synthetic.
OS Homo sapiens.
XX
PN WO2000068381-A1.
XX
PD 16-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12924.
XX
PR 11-MAY-1999; 99US-0309861.
XX
PA (ZIMO) ZIMOGENTICS INC.
XX
PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX
DR WPI: 2001-016096/02.
DR N-PSDB: AAA54474.
XX
PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
PT that stimulate proliferation or development of haematopoietic,
XX lymphoid and myeloid cells
XX
PS Example 17; Page 122-123; 134pp; English.
XX
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. These cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. A vector expressing a
CC secreted human zcytor 10 heterodimer is constructed. In this
CC construct the extracellular cytokine binding domain of zcytor 10
CC is fused to the heavy chain of IgG gamma and the extracellular
CC portion of the heteromeric cytokine receptor subunit (an
CC interleukin receptor subunit) is fused to human kappa light
CC chain (See GENESDB record AAA54474). The two sequences are fused
CC together using two primers (AAA54475, AAA54476).
CC
XX Sequence 106 AA:
SQ

```

Query Match 100.0%; Score 70; DB 22; Length 106;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 SSPVTKSFNRGEC 13
Db 94 sspvtksfnrgec 106

```

RESULT 8
 AAW40578
 ID AAW40578 standard; Protein: 107 AA.
 AC AAW40578;
 XX
 DT 21-JUL-1998 (first entry)
 XX
 DE Human kappa CL domain protein fragment.

KM Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;
KM disorder; salvage receptor binding epitope; cell adherence interaction;
KM lymphocyte; T cell inflammatory response.
XX
XX Homo sapiens.
XX
XX US5739277-A.
XX
XX
XX 14-APR-1998.
XX
XX 14-APR-1995; 9505-0422101.
XX
XX 14-APR-1995; 9505-0422101.
XX
XX (GETH) GENENTECH INC.
XX
XX Presta LG, Smedecor BR;
XX
XX WPI: 1998-250490/22.
XX
XX Polypeptide(s) that are not Fc fragments and have an increased
PT half-life - are useful for the treatment of LFA-1 mediated disorders
XX
XX
XX Disclosure; Fig 2: 38pp; English.
XX
XX This protein fragment is derived from a human immunoglobulin kappa CL
CC domain and is used to describe a novel method to produce polypeptides
CC which contain an epitope from the Fc region of an IgG molecule and a
CC mutated salvage receptor binding epitope. They are useful for the
CC treatment of LFA-1 mediated disorders. These are conditions caused by
CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,
CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence
CC in the polypeptides means that they have increased in vivo circulatory
CC half-lives when compared to normal Fc regions of IgG molecules.
XX
XX Sequence 107 AA:
SQ
Query Match 100.0%; Score 70; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSPYTKSFNRGEC 13
DB 95 ssptkspfngc 107
RESULT 9
AA50152
ID AAY50152 standard; Protein; 107 AA.
XX
XX AAY50152;
XX
XX 31-JAN-2000 (first entry)
XX
XX Human kappa light chain constant region.
XX
XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
KM humanisation; complementarily determining region; CDR; CDR grafting;
KM reshaped; reactive stroma; fibroblast; epithelial cancer;
KM diagnosis; immune response; framework sequence; constant region; lung;
KM variable region; productivity; treatment; cancer; colorectal; lung;
KM breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;
KM detection; wound healing; skin inflammation; tumour; immunogenicity;
KM light chain.
XX
XX Homo sapiens.
XX
XX EP953639-A1.
XX
XX 03-NOV-1999.
XX
XX 30-APR-1998; 98EP-0107925.
PF

XX
PR 30-APR-1998; 98EP-0107925.
XX
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
XX
XX PA
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
PI Rettig WJ;
XX
XX WPI: 1999-621833/54.
XX
XX N-PSDB; AA232777.
XX
XX New antibody protein, useful for treating cancer and for imaging
PT presence of activated stromal fibroblasts in healing wound or inflamed
PT skin -
XX
XX Disclosure; Fig 20: 143pp; English.
XX
XX This sequence represents a human kappa light chain, the cDNA of which
CC was used in the construction of a nucleotide encoding the light chain
CC of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number
CC HB 8269) is a murine monoclonal antibody against fibroblast
CC activation protein alpha (FAP). FAP is a cell surface molecule
CC of reactive stromal fibroblasts, and its induction is a highly
CC consistent molecular trait of the reactive stroma of many types of
CC epithelial cancer. Although F19 may be useful in vitro, e.g., for
CC diagnosis, its applications for in vivo use in humans are problematic
CC as it elicits a human anti-mouse response which reduces the efficacy of
CC the antibody in patients and impairs continued administration. The novel
CC human reshaped F19 was humanised by grafting the murine complementarity
CC determining regions (CDRs) of F19 onto human variable region framework
CC sequences, and then joining these "reshaped human" variable regions to
CC human constant regions. These modifications also result in the improved
CC producibility in eukaryotic cell culture systems as compared to a
CC chimeric antibody having the entire variable regions of F19 joined to
CC human constant regions. The human reshaped F19 antibody has low
CC immunogenicity for humans and is useful for treating cancers e.g.,
CC colorectal cancers, non-small cell lung cancers, breast cancers, head
CC and neck cancers, ovarian cancers, lung cancers, bladder cancers,
CC pancreatic cancers and metastatic cancers. It is also useful for the
CC detection of activated stromal fibroblasts in a healing wound, inflamed
CC skin or a tumour in a human patient.
XX
XX Sequence 107 AA:
SQ
Query Match 100.0%; Score 70; DB 20; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSPYTKSFNRGEC 13
DB 95 ssptkspfngc 107
RESULT 10
AAY08745
ID AAY08745 standard; Protein; 107 AA.
XX
XX AAY08745;
XX
XX 10-AUG-1999 (first entry)
XX
XX Human kappa-CL domain.
XX
XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
KM IgG4; kappa-CL domain; lambda-CL domain; focal ischemic stroke;
KM cerebroprotective; cerebral artery obstruction; blood flow; infarct;
KM CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
KM antibody.
XX
XX Homo sapiens.
XX
XX US5914112-A.
PN

[illegible]

XX		Production of antibody fragments with reduced renal clearance - by
PT		introducing salvage receptor binding epitope into CH1 or CL region
XX		
PS		Disclosure: Column 55-58; 38pp: English.
XX		
CC		This invention describes a method for preparing a variant Fab or F(ab') ₂
CC		polypeptide having increased half-life in vivo, where the polypeptide
CC		contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is
CC		cleared from the kidneys and does not contain an IgG Fc region. The
CC		method involves altering the polypeptide within the CH1 or CL region to
CC		incorporate a salvage receptor binding epitope taken from two loops of
CC		a CH2 domain of an IgG Fc region. The polypeptides have a reduced renal
CC		clearance rate and an increased circulatory half-life. This sequence
CC		represents a human kappa protein CL domain used in the method of the
CC		invention.
XX		
SQ		Sequence 107 AA:
XX		
Query Match	100.0%; Score 70;	DB 20; Length 107;
Best Local Similarity	100.0%; Pred. No. 4.1e-05;	
Matches 13;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
OY	1 SSPVTKSFNRGEC 13	
Db	95 ssyvltksfnrgcc 107	
RESULT 12		
AAB27000		
ID	AAB27000 standard; Protein: 107 AA.	
XX		
AC	AAB27000;	
XX		
DT	25-JAN-2001 (first entry)	
XX		
DE	Human kappa CL domain.	
XX		
KW	Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;	
RW	mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;	
KX	psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;	
XX	inflammation; vaccine.	
CS	Homo sapiens.	
FN	US6121022-A.	
PD	19-SEP-2000.	
XX		
Pf	14-APR-1995; 95US-0422112.	
XX		
PR	14-APR-1995; 95US-0422112.	
XX		
PA	(GETH) GENENTECH INC.	
PI	Presta LG, Snedecor BR;	
XX		
DR	WPI: 2000-610925/58.	
XX		
PT	New nucleic acid encoding new modified polypeptides with increased	
PT	circulatory half-life useful for preventing/treating LFA-1-mediated	
PT	disorders, e.g. reducing inflammatory responses or inducing tolerance	
PT	to immunostimulants _	
XX		
PS	Disclosure: Fig 2; 38pp: English.	
XX		
CC	The present sequence was used in a method for improving the in vivo	
CC	half-life of polypeptides. The polypeptides comprise an Ig constant	
CC	domain or an Ig-like constant domain, and a salvage receptor binding	
CC	epitope within the Ig or Ig-like domain. The salvage receptor epitope is	
CC	taken from two loops of the CH2 domain of an Fc region of an Ig molecule.	
CC	The modified polypeptides are useful for preventing or treating	

CC LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis,
 CC allergic conditions (e.g. eczema); antigen-antibody complex mediated
 CC diseases, B-cell lymphomas. They are also useful for wound repair,
 CC reducing inflammatory responses and inducing tolerance to
 CC immunostimulants. They may also be used in diagnostic assays. The nucleic
 CC acids and modified polypeptides are useful for the passive immunisation
 CC of patients, as well as for affinity purification of an antigen from
 CC recombinant cell culture or natural sources.
 CC
 XX Sequence 107 AA:

Query Match 100.0%; Score 70; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
 |||||
 DB 95 ssptksfngrec 107

RESULT 13
 AAB62265
 ID AAB62265 standard; Protein; 107 AA.
 XX
 AC AAB62265;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Light chain construct A31A amino acid fragment.
 XX
 KM Fusion protein; cell surface antigen; cancer; monoclonal antibody;
 KM light chain construct; carcinogenic.
 XX
 OS Mammalia.
 OS
 PN WO200119842-A1.
 PN
 XX
 PD 22-MAR-2001.
 PD
 XX
 PF 18-SEP-2000; 2000WO-US25558.
 PF
 XX
 PR 17-SEP-1999; 99US-0399079.
 PR
 XX
 PA (GENZ) GENZYME TRANSGENICS CORP.
 PA
 PI Pollock D, Meade HM, Bosslet K;
 PI
 XX
 DR WPI: 2001-257871/26.
 DR
 XX
 DR N-PSDB: AAF57571.
 DR

PT New fusion protein, useful for killing diseased cells e.g. cancer
 PT cells, comprises fused first and second units, such that the protein
 PT assembles into complex which optimizes activity of multimeric form of
 PT second unit -
 XX
 PS Example 1; Fig 1B: 88pp; English.

CC The invention relates to a fusion protein (I) comprising a first member
 CC fused to a second member, where the first and second members are chosen
 CC such that (I) assembles into a complex having a number of subunits which
 CC optimizes activity of the multimeric form of the second member. (I) is
 CC useful for selectively killing an aberrant or diseased cell which
 CC expresses a target antigen on its surface, e.g., a cancer cell expressing
 CC a cell surface antigen. (I) is also useful for detecting in vitro or in
 CC vivo the presence of target antigen in a sample, e.g., for diagnosing a
 CC disease, by contacting a sample or a control sample that allows
 CC interaction of (I) which is labeled, and detecting formation of a
 CC complex. (I) is also useful for selectively directing (e.g., localizing)
 CC the second unit of (I) to the vicinity of an undesirable cell. The
 CC present sequence represents a fragment of a light chain construct A31A
 CC that was generated using the light chain sequence from a humanised Mab
 CC against carcinoembryonic antigen (431).

XX
 SO Sequence 107 AA:

Query Match 100.0%; Score 70; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
 |||||
 DB 95 ssptksfngrec 107

RESULT 14
 AAW70802
 ID AAW70802 standard; Protein; 108 AA.
 XX
 AC AAW70802;
 XX
 DT 03-FEB-1999 (first entry)
 XX
 DE Amino acid sequence of the kappa domain.
 XX
 KM gp130; cytokine antagonist; interleukin; gamma-interferon;
 KM granulocyte macrophage colony-stimulating factor; J peptide;
 KM transforming growth factor-beta.
 XX
 OS Synthetic.
 OS
 PN US5844099-A.
 PN
 XX
 PD 01-DEC-1998.
 PD
 XX
 PF 27-NOV-1995; 95US-0563105.
 PF
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR
 XX
 PR 20-OCT-1993; 93US-0140222.
 PR
 XX
 PA (REGG-) REGENERON PHARM INC.
 PA
 PI Economides A, Stahl N, Yancopoulos GD;
 PI
 XX
 DR WPI: 1999-044669/04.
 DR
 XX
 PT Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 13; 46pp; English.

CC The present sequence represents the amino acid sequence of
 CC kappa domain. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 CC
 XX Sequence 108 AA:

Query Match 100.0%; Score 70; DB 20; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
 |||||

Db 96 sspvtsfmgrec 108

RESULT 15
 AAY92191
 ID AAY92191 standard; protein; 108 AA.
 XX
 AC AAY92191;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Human IgG1 kappa domain.
 XX
 KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;
 XX cytosolic; immunomodulator; osteopathic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..2
 FT /note= "Ser-gly bridge"
 FT Domain 3..107
 FT /label= kappa_domain
 XX
 PN W0200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI; 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 4; Flg 13; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 70; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSPVTKSFNRGEC 13
 |||||||||
 Db 96 sspvtsfmgrec 108

Search completed: January 4, 2002, 18:09:11
 Job time: 276 sec

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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:37 ; Search time 19.66 Seconds

(without alignments)
14.880 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPYTKSFNRREC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCPUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/BACKFILES1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	106	2	US-08-378-939-40
2	70	100.0	106	2	US-08-378-939-42
3	70	100.0	106	2	US-08-761-277A-49
4	70	100.0	106	3	US-08-444-644-26
5	70	100.0	107	1	US-08-422-101-8
6	70	100.0	107	1	US-08-422-091-8
7	70	100.0	107	2	US-08-422-092-8
8	70	100.0	107	2	US-08-788-800-5
9	70	100.0	107	3	US-08-422-093-8
10	70	100.0	107	3	US-08-422-112-8
11	70	100.0	143	1	US-08-236-311-10
12	70	100.0	143	3	US-08-437-918-10
13	70	100.0	213	3	US-08-630-820-6
14	70	100.0	213	3	US-08-397-411-12
15	70	100.0	214	1	US-08-425-763-1
16	70	100.0	214	1	US-08-253-877C-5
17	70	100.0	214	1	US-08-458-516-12
18	70	100.0	214	2	US-07-934-373C-24
19	70	100.0	214	2	US-07-934-373C-39
20	70	100.0	214	2	US-07-934-373C-40
21	70	100.0	214	2	US-08-480-753-6
22	70	100.0	214	2	US-08-452-164A-5
23	70	100.0	214	2	US-08-788-800-11
24	70	100.0	214	3	US-09-041-889-11
25	70	100.0	214	3	US-08-437-642B-24
26	70	100.0	214	3	US-08-437-642B-39
27	70	100.0	214	3	US-08-437-642B-40

28	70	100.0	214	3	US-08-811-757-1	Sequence 1, Appl
29	70	100.0	214	3	US-08-837-058-11	Sequence 11, Appl
30	70	100.0	214	3	US-09-097-309-2	Sequence 2, Appl
31	70	100.0	214	3	US-08-397-411-5	Sequence 5, Appl
32	70	100.0	214	4	US-09-097-171A-2	Sequence 2, Appl
33	70	100.0	214	4	US-09-249-230-1	Sequence 1, Appl
34	70	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appl
35	70	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appl
36	70	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appl
37	70	100.0	215	2	US-08-480-753-8	Sequence 8, Appl
38	70	100.0	218	2	US-08-887-352B-13	Sequence 13, Appl
39	70	100.0	218	2	US-08-887-352B-15	Sequence 15, Appl
40	70	100.0	218	2	US-08-887-352B-17	Sequence 17, Appl
41	70	100.0	218	2	US-08-887-352B-19	Sequence 19, Appl
42	70	100.0	218	2	US-08-887-352B-24	Sequence 24, Appl
43	70	100.0	218	3	US-08-466-151-9	Sequence 9, Appl
44	70	100.0	218	4	US-09-109-207C-13	Sequence 13, Appl
45	70	100.0	218	4	US-09-109-207C-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-378-939-40
; Sequence 40, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-40

Query Match 100.0%; Score 70; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SSPYTKSFNRREC 13
|||||

Db 94 SSPVTKSFNRGEC 106

RESULT 2

US-08-378-939-42

Sequence 42, Application US/08378939

Patent No. 5876961

GENERAL INFORMATION:

APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

STREET: 555 THIRTEENTH ST. N.W.

CITY: WASHINGTON

STATE: D. C.

COUNTRY: U.S.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,939

FILING DATE:

CLASSIFICATION: 439

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-939-42

Query Match 100.0%; Score 70; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVTKSFNRGEC 106

RESULT 3

US-08-761-277A-49

Sequence 49, Application US/08761277A

Patent No. 5972334

GENERAL INFORMATION:

APPLICANT: Denney Jr., Dan W.

TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And

TITLE OF INVENTION: Leukemia

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Cartoll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/761,277A

FILING DATE: 06-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/644,664

FILING DATE: 01-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: GENITOPE-02406

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-761-277A-49

Query Match 100.0%; Score 70; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVTKSFNRGEC 106

RESULT 4

US-08-444-644-26

Sequence 26, Application US/08444644

Patent No. 6015555

GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millita Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,644

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,246

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-NOV-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PC/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-444-644-26

Query Match 100.0%; Score 70; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
|||||
Db 94 SSPVTKSFNRGEC 106

RESULT 5
US-08-422-101-8
Sequence 8, Application US/08422101
Patent No. 5739277
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,101
FILING DATE: 14-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-101-8

Query Match 100.0%; Score 70; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPVTKSFNRGEC 13
|||||
Db 95 SSPVTKSFNRGEC 107

RESULT 6
US-08-422-091-8
Sequence 8, Application US/08422091
Patent No. 5747035
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,091
FILING DATE: 14-APR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-091-8

Query Match 100.0%; Score 70; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
|||||
Db 95 SSPVTKSFNRGEC 107

RESULT 7
US-08-422-092-8
Sequence 8, Application US/08422092
Patent No. 5869046
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,092
FILING DATE: 14-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-092-8
Query Match 100.0%; Score 70; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPVTKSFNRGEC 13
|||||
Db 95 SSPVTKSFNRGEC 107
RESULT 8
US-08-788-800-5
Sequence 5, Application US/08788800
Patent No. 591412
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-788-800-5
Query Match 100.0%; Score 70; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPVTKSFNRGEC 13
|||||
Db 95 SSPVTKSFNRGEC 107
RESULT 9
US-08-422-093-8
Sequence 8, Application US/08422093
Patent No. 6096871
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,093
FILING DATE: 14-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-093-8
Query Match 100.0%; Score 70; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSPVTKSFNRGEC 13
|||||
Db 95 SSPVTKSFNRGEC 107

RESULT 10
US-08-422-112-8
; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: palin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,112
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-112-8

Query Match 100.0%; Score 70; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
DB 95 SSPVTKSFNRGEC 107

RESULT 11
US-08-236-311-10
; Sequence 10, Application US/08236311.
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-10

Query Match 100.0%; Score 70; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
DB 131 SSPVTKSFNRGEC 143

RESULT 12
US-08-457-918-10
; Sequence 10, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: palin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 143 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-457-918-10

Query Match 100.0%; Score 70; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
Db 131 SSPVTKSFNRGEC 143

RESULT 13
US-08-630-820-6
Sequence 6, Application US/08630820
Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: OPPER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-820-6

Query Match 100.0%; Score 70; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
Db 201 SSPVTKSFNRGEC 213

RESULT 14
US-08-397-411-12
Sequence 12, Application US/08397411
Patent No. 6126914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-12

Query Match 100.0%; Score 70; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

DB 201 SSPVTKSFNRGEC 213

RESULT 15

US-08-425-763-1
 ; Sequence 1, Application US/08425763
 ; Patent No. 5641870
 ; GENERAL INFORMATION:
 ; APPLICANT: Rinderknecht, Ernst H.
 ; APPLICANT: Zapata, Gerardo A.
 ; TITLE OF INVENTION: ANTIBODY PURIFICATION
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/425,763
 ; FILING DATE: 20-APR-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 00,000
 ; REFERENCE/DOCKET NUMBER: 941
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 214 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ;
 ; US-08-425-763-1

Query Match 100.0%; Score 70; DB 1; Length 214;
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
 DB 202 SSPVTKSFNRGEC 214

Search completed: January 4, 2002, 18:09:37
 Job time: 252 sec

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A:Contents: Bence Jones protein T1
 A:Accession: A91651
 A:Molecule type: protein
 A:Residues: 1-106 <SUT>
 R:Heier, P.A.; Max, E.E.; Seidman, J.G.; Melzel Jr., J.V.; Leder, P.
 Cell 22, 197-207, 1980
 A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
 A:Reference number: A90806; MUID:81042304
 A:Accession: A90806
 A:Molecule type: DNA
 A:Residues: 1-106 <HE>
 A:Cross-references: GB:00241; NID:933140; PIDN:CA23823.1; PID:91335148
 A:Note: the sequence was determined from the germ-line gene
 R:Hiltschmann, N.; Bernikol, H.U.; Hess, M.; Langer, B.; Ponslingl, H.; Steinmetz-Kayne,
 In Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
 A:Reference number: A94417
 A:Contents: Bence Jones protein Roy
 A:Accession: A94417
 A:Molecule type: protein
 A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>
 A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
 R:Hiltschmann, N.
 Hope-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
 A:Title: Die volstandige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (Kappa-Typ).
 A:Reference number: A91639; MUID:68242255
 A:Contents: Bence Jones protein Cum
 A:Accession: A91639
 A:Molecule type: protein
 A:Residues: 1-56, 'Q', 58-106 <H12>
 R:Ritani, K.; Shinoda, T.; Putnam, F.W.
 J. Biol. Chem. 244, 3550-3560, 1969
 A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
 A:Reference number: A92047; MUID:69234734
 A:Contents: Bence Jones protein Ag
 A:Accession: A92047
 A:Molecule type: protein
 A:Residues: 1-13, 'N', 15-106 <RT>
 R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
 Science 169, 56-59, 1970
 A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
 A:Reference number: A94242; MUID:70201507
 A:Contents: Waldenstrom's macroglobulin Ou
 A:Accession: A94242
 A:Molecule type: protein
 A:Residues: 1-13, 'N', 15-106 <KOH>
 R:Kurtz, J.H.; Bowcock, A.M.; Erllich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
 Am. J. Hum. Genet. 48, 613-620, 1991
 A:Title: Km typing with PCR: application to population screening.
 A:Reference number: A37927; MUID:91150772
 A:Accession: B37927
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 8-106 <KUR>
 A:Note: allozyme Inv(3)
 R:Steiner, V.; Chang, J.Y.
 FEBS Lett. 222, 6-10, 1987
 A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
 A:Reference number: S02572; MUID:88005152
 A:Contents: annotation
 C:Genetics:
 A:Gene: GDB:IGKC
 A:Cross-references: GDB:120086; OMIM:147200
 A:Map position: 2p12-2p12
 C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kap
 hain disulfide bonds: in some cases, such as IGA and IGM, the subunits associate into 16
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:19-88/Domain: immunoglobulin homology <IMW>
 F:26-86/Disulfide bonds: #status experimental
 F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 100.0%; Score 70; DB 1; Length 106;

Best Local Similarity 100.0%; Pred. NO. 3.5e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSPVTKSFNRGEC 13
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 Db 94 SSPVTKSFNRGEC 106

RESULT 3
 S52059
 JC-Kappa protein - human
 C:Species: Homo sapiens (man)
 C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
 C:Accession: S52059
 R:Frances, V.; Pandreu-Garcia, D.; Gurec, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland,
 EMBO J. 13, 5937-5943, 1994
 A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy
 A:Reference number: S52059; MUID:95112804
 A:Accession: S52059
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <FRA>
 C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 100.0%; Score 70; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 4.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
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 Db 123 SSPVTKSFNRGEC 135

RESULT 4
 JE0244
 Ig kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0244
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazl, H.
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL
 A:Reference number: JE0243
 A:Accession: JE0244
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 70; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
 |||
 Db 203 SSPVTKSFNRGEC 215

RESULT 5
 JE0242
 Ig kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0242
 R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
 submitted to JIPID, November 1998
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
 A:Reference number: JE0241
 A:Accession: JE0242
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
|||||
Db 203 SSPVTKSFNRGEC 215

RESULT 6

JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (YKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
|||||
Db 203 SSPVTKSFNRGEC 215

RESULT 7

JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu]
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
|||||
Db 204 SSPVTKSFNRGEC 216

RESULT 8

A23746
Ig kappa chain V-III (KAV cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immun
A:Reference number: A23746; MUID:91131575

A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 61; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGE 12
|||||
Db 203 SSPVTKSFNRGE 214

RESULT 9

S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42772
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75336; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 61; DB 2; Length 217;
Best Local Similarity 76.9%; Pred. No. 0.00041;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
|||||
Db 205 TSPVTKSFNRGEC 217

RESULT 10

S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porph
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphy
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'N', 3-212 <TAM>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 87.1%; Score 61; DB 2; Length 218;
Best Local Similarity 76.9%; Pred. No. 0.00041;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
Db 206 TSPIVKSFNREGC 218

RESULT 11

S38865

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001

C:Accession: S38865

R:Klpp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of an

A:Reference number: S38864

A:Accession: S38865

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <KIP>

A:Cross-references: EMBL:227396; NID:9416538; PIDN:CAA81787.1; PID:9416539

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 87.1%; Score 61; DB 2; Length 219;
Best Local Similarity 76.9%; Pred. No. 0.00041;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 207 TSPIVKSFNREGC 219

RESULT 12

K1RTB

Ig kappa chain C region (allele b) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 28-May-1999

C:Accession: A93901; A92807; A02117

R:Sheppard, H.W.; Gutman, G.A.

Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A>Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the I

A:Reference number: A93901; MUID:82082587

A:Accession: A93901

A:Molecule type: DNA

A:Residues: 1-106 <SHE>

A:Cross-references: GB:J01241; GB:J00745; GB:J02574; GB:J02575; NID:957849; PIDN:CAA2455

A:Experimental source: strain LOU

R:Starace, V.; Querinjean, P.

J. Immunol. 115, 59-62, 1975

A>Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation

A:Reference number: A92807; MUID:75212228

A:Contents: Bence Jones protein S211

A:Accession: A92807

A:Molecule type: protein

A:Residues: 1, 'N', 'K', '31-47', '49-78', '80-86', '88-98', '99', '101-106 <STA>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ig

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer

F:19-88/Domain: Immunoglobulin homology <IMM>

F:26-86/Disulfide bonds: #status predicted.

F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 84.3%; Score 59; DB 1; Length 106;

Best Local Similarity 84.6%; Pred. No. 0.00046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
Db 94 SSPVKSFNREGC 106

RESULT 13

K1RTA

Ig kappa chain C region (allele a) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 22-Jun-1999

C:Accession: A02118

R:Sheppard, H.W.; Gutman, G.A.

Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A>Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the

A:Reference number: A93901; MUID:82082587

A:Accession: A02118

A:Molecule type: DNA

A:Residues: 1-106 <SHE>

A:Cross-references: GB:J02574; GB:J00745; NID:9204820; PIDN:AAA1411.1; PID:9204821

A:Experimental source: strain DA

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer

F:19-88/Domain: immunoglobulin homology <IMM>

F:26-86/Disulfide bonds: #status predicted

F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 84.3%; Score 59; DB 1; Length 106;
Best Local Similarity 84.6%; Pred. No. 0.00046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVKSFNREGC 106

RESULT 14

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A>Title: Nucleotide sequence of Ig-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c

A:Reference number: S06084; MUID:90016888.

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <ANT>

F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 59; DB 2; Length 240;
Best Local Similarity 84.6%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 228 SSPVKSFNREGC 240

RESULT 15

KIMS

Ig kappa chain C region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1980 #sequence_revision 17-Dec-1982 #text_change 16-Aug-1996
 C:Accession: B90262; A90778; B93736; A92322; A93748; A02119
 R:Swastl, J.; Milstein, C.
 Biochem. J. 128, 427-444, 1972
 A:Title: The complete amino acid sequence of a mouse kappa light chain.
 A:Reference number: A90262; MUID:73053310
 A:Contents: myeloma protein MOPC 21
 A:Accession: B90262
 A:Molecule type: Protein
 A:Residues: 1-52, BSRZMB, 60-106 <SVA>
 R:Swastl, J.; Milstein, C.
 Biochem. J. 126, 837-850, 1972
 A:Title: The disulphide bridges of a mouse immunoglobulin G1 protein.
 A:Reference number: A90259; MUID:73008869
 A:Contents: annotation: MOPC 21, disulfide bonds
 A:Note: Cys-106 is involved in a light-heavy chain bond
 R:Hamlyn, P.H.; Brownlee, G.G.; Cheng, C.C.; Galt, M.J.; Milstein, C.
 Cell 15, 1067-1075, 1978
 A:Title: Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA
 A:Reference number: A90778; MUID:79084137
 A:Accession: A90778
 A:Molecule type: mRNA
 A:Residues: 1-106 <HAM>
 R:Hamlyn, P.H.; Galt, M.J.; Milstein, C.
 Nucleic Acids Res. 9, 4485-4494, 1981
 A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideo
 A:Reference number: A93736; MUID:82059477
 A:Contents: MOPC 21
 A:Accession: B93736
 A:Molecule type: mRNA
 A:Residues: 1-106 <HA2>
 R:Max, E.E.; Maizel Jr., J.V.; Leder, P.
 J. Biol. Chem. 256, 5116-5120, 1981
 A:Title: The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kapp
 A:Reference number: A92322; MUID:81191915
 A:Accession: A92322
 A:Molecule type: DNA
 A:Residues: 1-106 <MAX>
 A:Note: The sequence was determined from the germline gene
 R:Altenburger, W.; Neumaler, P.S.; Steinmetz, M.; Zachau, H.G.
 Nucleic Acids Res. 9, 971-981, 1981
 A:Title: DNA sequence of the constant gene region of the mouse immunoglobulin kappa cha
 A:Reference number: A93748; MUID:81198949
 A:Accession: A93748
 A:Molecule type: DNA
 A:Residues: 1-106 <ALT>
 A:Note: The sequence was determined from the germline gene
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:26-86/Disulfide bonds: #status experimental

Query Match 78.6%; Score 55; DB 1; Length 106;
 Best Local Similarity 69.2%; Pred. No. 0.0027;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13
 :||| ||||| ||
 DB 94 TSPIVKSFNRNEC 106

Search completed: January 4, 2002, 18:10:05
 Job time: 225 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:14:37 ; Search time 15.29 Seconds
(without alignments)
31.173 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPVTKSFNNGEC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	106	1 KAC_HUMAN	P01834 homo sapien
2	59	84.3	106	1 KACA_RAT	P01836 rattus norv
3	59	84.3	106	1 KACB_RAT	P01835 rattus norv
4	55	78.6	106	1 KAC_MOUSE	P01837 mus musculu
5	54	77.1	106	1 KACB_RABIT	P01839 oryctolagus
6	44	62.9	103	1 KAC4_RABIT	P01840 oryctolagus
7	42	60.0	104	1 KAC9_RABIT	P01838 oryctolagus
8	42	60.0	121	1 YCWL_YEAST	P25642 saccharomyc
9	40.5	57.9	772	1 GELS_PIG	P20305 sus scrofa
10	39	55.7	104	1 KAC6_RABIT	P03984 oryctolagus
11	38	54.3	657	1 MRB_DROME	P04197 drosophila
12	37	52.9	455	1 MURE_BUCAL	P57315 buchneria ap
13	37	52.9	895	1 YAS4_METUA	P05854 methanococc
14	36	51.4	177	1 CHRI_BOOMO	P13532 bombyx mori
15	36	51.4	354	1 MTD2_HERAU	P25265 herpetosiph
16	36	51.4	637	1 RES1_SCHRO	P33520 schizosacch
17	36	51.4	715	1 ADSV_MOUSE	P06004 mus musculu
18	36	51.4	1057	1 RPOC_STAUA	P47770 staphylococ
19	36	51.4	1444	1 RRLP_RDVA	P02119 rice dwarf
20	36	51.4	1444	1 RRLP_RDVE	P09831 rice dwarf
21	35.5	50.7	730	1 GELS_HORSE	P28372 equus cabal
22	35.5	50.7	782	1 GELS_HORSE	P06365 homo sapien
23	35	50.0	73	1 YDBF_SCHRO	P01065 schizosacch
24	35	50.0	73	1 NTL1_KACAN	P01385 acanthophis
25	35	50.0	392	1 DCAV_LELIN	P09640 leishmania
26	35	50.0	492	1 SECV_CVAPA	P25014 cyanophora
27	35	50.0	598	1 BCCA_MYCLE	P46392 mycobacteri
28	35	50.0	625	1 BAR3_SCHCO	P56502 schizosacch
29	35	50.0	715	1 ADSV_BOVIN	P02804 bos taurus
30	35	50.0	715	1 ADSV_HUMAN	P09643 xenopus lae
31	35	50.0	760	1 OCPL_XENLA	P09643 xenopus lae
32	35	50.0	1069	1 C910_HUMAN	P09643 xenopus lae
33	35	50.0	1736	1 ZOL_HUMAN	P07157 homo sapien

34	35	50.0	1745	1 ZOL_MOUSE	P39447 mus musculu
35	35	50.0	1782	1 VITR_BOOMO	P02730 bombyx mori
36	34.5	49.3	96	1 RL21_METTH	P02737 methanobact
37	34	48.6	279	1 PHEX_LACLA	P43909 lactococcus
38	34	48.6	292	1 YOW1_CAEEL	P30647 caenorhabdi
39	34	48.6	397	1 CAPB_BACAN	P19580 bacillus an
40	34	48.6	826	1 VILL_HUMAN	P09327 homo sapien
41	34	48.6	826	1 VILL_MOUSE	P06268 mus musculu
42	34	48.6	1004	1 RPOC_OENOE	P95405 oenococcus
43	34	48.6	1053	1 RPOC_LISIN	P7879 lysteria in
44	34	48.6	1077	1 XYNV_CLOTM	P51584 clostridium
45	34	48.6	1355	1 CA21_RANCA	O42350 rana catesb

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	106 AA.
KAC_HUMAN				
ID	KAC_HUMAN			
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	IG KAPPA CHAIN C REGION.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MWELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RT	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RT	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hieber P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RT	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess W., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(in) Finek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press,			
RL	New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."			

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE-69234734; Pubmed-4893682;
RA Titani K., Shioda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RL complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OJ).
RX MEDLINE-70201507; Pubmed-5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RL chains."; Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA 6 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC -----
DR EMBL: J00241; AAA58989.1; -
DR EMBL: V00557; CAA23823.1; -
DR PIR: A02116; K3HU.
DR MTM: 147200; -
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl.1.
DR PROSITE: PS00290; IG_MHC.1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT VARIANT /FTID-VAR.003897
FT CONFLICT 14 14 D->N (IN REF. 7 AND 8).
FT CONFLICT 37 37 E->Q (IN REF. 5 AND 6).
FT CONFLICT 57 57
SQ SEQUENCE 106 AA; 11609 MW; 51984D1PDD372CE8 CRC64;

Query Match 100.0%; Score 70; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSPVTKSFNRGEC 13
Db 94 SSPVTKSFNRGEC 106

RESULT 2
KACB_RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN C REGION, A ALLELE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-DA;
RX MEDLINE-82082587; Pubmed-6273908;
RA Sheppard H.W., Gutman G.A.;
```

```
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
DR PIR: A02118; K1RTA.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl.1.
DR PROSITE: PS00290; IG_MHC.1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT DISULFID 106 106
SQ SEQUENCE 106 AA; 11732 MW; B7E120970DDDD6 CRC64;

Query Match 84.3%; Score 59; DB 1; Length 106;
Best Local Similarity 84.6%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSPVTKSFNRGEC 13
Db 94 SSPVTKSFNRGEC 106

RESULT 3
KACB_RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN C REGION, B ALLELE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-LOU;
RX MEDLINE-82082587; Pubmed-6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE-75212238; Pubmed-807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes.";
RL J. Immunol. 115:59-62(1975).
DR PIR: A02117; K1RTB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl.1.
DR PROSITE: PS00290; IG_MHC.1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT DISULFID 106 106
FT CONFLICT 2 2 D->N (IN REF. 2).
FT CONFLICT 30 30 N->K (IN REF. 2).
FT CONFLICT 48 48 MISSING (IN REF. 2).
FT CONFLICT 79 79 E->Q (IN REF. 2).
FT CONFLICT 87 87 E->Q (IN REF. 2).
FT CONFLICT 98 98 V->W (IN REF. 2).
FT CONFLICT 100 100 S->N (IN REF. 2).
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;

Query Match 84.3%; Score 59; DB 1; Length 106;
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Best Local Similarity 84.6%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13

DB 94 SSPVTKSFNRNEC 106

RESULT 4

KAC_MOUSE STANDARD: PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN C REGION.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
RN [3]
RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Mollemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
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CC EMBL: V00807; CAA24189.1; -
DR PIR: A02119; KIMS.
DR PIR: S01320; S01320.
DR MGI: 96495; I9K-C.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl.1.
DR PROSITE: PS00290; Ig_MHC.1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT DISULFID 106 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51F5EF49BA85 CRC64;
INTERCHAIN (WITH A HEAVY CHAIN).

Query Match 78.6%; Score 55; DB 1; Length 106;
Best Local Similarity 69.2%; Pred. No. 0.0011;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13

DB 94 TSPVTKSFNRNEC 106

RESULT 5

KACB_RABIT STANDARD: PRT; 106 AA.
ID KACB_RABIT
AC P01839;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA-B4 CHAIN C REGION.
GN K-BAS.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BASILEA.
RA Heidmann O., Rougeon F.;
RT "Multiplicity of constant kappa light chain genes in the rabbit genome: a b4b4 homozygous rabbit contains a kappa-bas gene.";
RL EMBO J. 2:437-441(1983).
CC -I- MISCELLANEOUS: IN BASILEA RABBITS, THE MAJOR TYPE OF LIGHT CHAIN IS LAMBDA. THE KAPPA CHAIN SHOWN IS A MINOR COMPONENT. ALL OTHER RABBIT B ALLOTYPES HAVE 64-CYS.
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CC or send an email to license@isb-sib.ch).

FT	DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
SEQUENCE	106 AA;	11279 MW;	AC9B928DDA853849	CRC64.
Query Match		77.1%;	Score 54;	DB 1;
Best Local Similarity		61.5%;	Pred. No. 0.0018;	
Matches	8;	Conservative	4;	Mismatches 1;
				Indels 0;
				Gaps 0;
Qy	1 SSPVTKSFNRGEC	13		
	11:11111111			
Db	94 ASPVQSFNRGDC	106		
RESULT	6			
KAC4_RABIT	STANDARD:	PRT:	103 AA.	
AC	P01840;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA-B4 CHAIN C REGION			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=83300036; PubMed=6412231;			
RA	Emorine L., Dreher K.L., Kindt T.J., Max E.E.;			
RT	"Rabbit immunoglobulin kappa genes: structure of a germline b4			
RT	allele type J-C locus and evidence for several b4-related sequences in			
RL	the rabbit genome.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=82060334; PubMed=6795636;			
RA	Heizmann O., Auffray C., Cazenave P.-A., Rougeon F.;			
RT	"Nucleotide sequence of constant and 3' untranslated regions of a			
RT	kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).			
RN	[3]			
RP	SEQUENCE.			
RA	MEDLINE=75133568; PubMed=1091650;			
RA	Chen K.C.S., Kindt T.J., Krause R.M.;			
RT	"Primary structure of the L chain from a rabbit homogeneous antibody			
RT	to streptococcal carbohydrate. II. Sequence determination of peptides			
RL	from tryptic and peptic digests.";			
RL	J. Biol. Chem. 250:3289-3296(1975).			
CC	-1- SPECIELLADEOS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE			
CC	MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE			
CC	SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM			
CC	THE SERUM OF A SINGLE RABBIT.			
CC	-----			
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CC	-----			
DR	EMBL: X00231; CAA25051.1; -.			
DR	PIR: A02122; KARB.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003597; Ig_cl.			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART: SM00407; IGC1; J.			
DR	PROSITE: PS00290; Ig_MHC; FALSE_NEG.			
KW	Immunoglobulin domain; Immunoglobulin C region.			
FT	NON_TER	1		
FT	DISULFID	26	85	
FT	DISULFID	103	103	INTERCHAIN (WITH A HEAVY CHAIN).
FT	CONFLICT	58	58	N -> D (IN REF. 3)
FT	SEQUENCE	103 AA;	11043 MW;	5FC5ACCB8606E8DB CRC64;

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Query Match Similarity      62.9%; Score 44; DB 1; Length 103;
Best Local Similarity      53.8%; Pred. No. 0.15;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY      1 SSPVTKSFNRGEC 13
      : : | : ||||| : |
DB      91 TTSVVSFNRGDC 103

RESULT 7
KAC9_RABIT STANDARD: PRT; 104 AA.
ID_KAC9_RABIT
AC P01838;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA-B9 CHAIN C REGION.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=76176480; PubMed=817288;
RA Farnsworth V., Goodflesh R., Rodkey S., Hood L.;
RA "Immunoglobulin allotypes of rabbit kappa chains: polymorphism of a
RA control mechanism regulating closely linked duplicated genes?";
RL Proc. Natl. Acad. Sci. U.S.A. 73:1293-1296(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM POOLED IMMUNOGLOBULIN
CC OF HOMODYGCOUS B9 RABBITS.
DR PIR: A02120; K9RB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_CL.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl_1.
DR PROSITE: PS00290; Ig_MHC; FALSE_NEG.
DR Immunoglobulin domain;
KW NON_TER 1
FT DISULFID 27 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 104 104
SQ SEQUENCE 104 AA; 11347 MW; 427B1668B0EC8D98 CRC64;

Query Match      60.0%; Score 42; DB 1; Length 104;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY      4 VTKSFNRGEC 13
      : : ||||| : |
DB      95 IYVSFNRGDC 104

RESULT 8
YCW1_YEAST STANDARD: PRT; 121 AA.
ID_YCW1_YEAST
AC P25642;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYDROTHERMAL 13.6 KDA PROTEIN IN CPRA-SSK22 INTERGENIC REGION.
GN YCR071C OR YCR71C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Sacchariomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Ballester J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
RA Sanz E.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: SOME, TO S.POMBE SPAC3H8.03.

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 CC -----
 DR EMBL: K01363; AAA31355.1; -.
 DR PIR: A02124; KSRBV.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00407; Igc1: 1.
 DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DISULFID 26 85
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;
 Query Match 55.7%; Score 39; DB 1; Length 104;
 Best Local Similarity 58.3%; Pred. No. 1.4;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 SPVTKSFNRKC 13
 Db 93 SPVQSFNRKNC 104
 ID MYB_DROME STANDARD; PRT: 657 AA.
 AC P04197; Q9VXW9;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE MYB PROTEIN
 GN MYB OR CG9045.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=88082681; PubMed=3121304;
 RA Peters C.W.B., Sippel A.E., Vingron M., Klempner K.-H.;
 RT "Prosohila and vertebrate myb proteins share two conserved regions,
 RL one of which functions as a DNA-binding domain.";
 RL EMBO J. 6:3085-3090(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731137;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailev R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paolis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matile B., McIntosh T.C., McLeod M.P., Mpherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclat J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 1-441 FROM N.A.
 RX MEDLINE=85176969; PubMed=3921261;
 RA Katzen A.L., Kornberg T.B., Bishop J.M.;
 RL Cell 41:449-456(1985).
 CC -1- FUNCTION: MYB IS A DNA-BINDING PROTEIN THAT SPECIFICALLY
 CC RECOGNIZES THE SEQUENCE 5'-YAAC(G/T)G-3'.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY.
 CC -----
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 CC -----
 DR EMBL: X05939; CA29373.1; -.
 DR EMBL: AE003500; AAF48529.1; -.
 DR EMBL: M11281; AAA70367.1; -.
 DR PIR: S00578; TYFEMA.
 DR HSP: P06876; IMB1.
 DR FlyBase: FBgn0002914; Myb.
 DR InterPro: IPR001005; Myb_DNA_bind.
 DR Pfam: PF00249; myb_DNA-binding; 3.
 DR SMART: SM00395; SANT; 3.
 DR PROSITE: PS00037; MYB_1; 3.
 DR PROSITE: PS00334; MYB_2; 3.
 DR PROSITE: PS50090; MYB_3; 3.
 DR Nuclear protein; DNA-binding; Repeat.
 KW DNA_BIND 79 130 MYB.
 FT DNA_BIND 131 182 MYB.
 FT DNA_BIND 183 233 MYB.
 FT CONFLICT 370 370 OL -> V (IN REF. 1).
 FT CONFLICT 440 441 QL -> KY (IN REF. 3).
 SQ SEQUENCE 657 AA; 74045 MW; 8265B37ABB250A2A CRC64;
 Query Match 54.3%; Score 38; DB 1; Length 657;
 Best Local Similarity 70.0%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SSPVTKSFNR 10
 Db 410 STPVTKYINR 419
 ID MYB_BUCAL STANDARD; PRT: 455 AA.
 AC P57315;
 RESULT 12
 MURF_BUCAL
 ID MURF_BUCAL
 AC P57315;

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RA MEDLINE=96337999; PubMed=8688087; RA Flutschmann R.D.,
RA Bult C.J., White O., Olsen G.J., Zhou L., RA
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kereyagbe A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weissbrock K.G., Merrick J.M., Glodok A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii."
RA Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE UDP-GLUCOSE/GDP-MANNOSE DEHYDROGENASES
CC FAMILY.
CC -----
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CC -----
CC DR EMBL: U67548; AAB99056.1; -.
CC DR TIGR; MJ1054; -.
CC DR InterPro: IPR003586; HincC.
CC DR InterPro: IPR003587; HincN.
CC DR InterPro: IPR002055; NAD_binding.
CC DR InterPro: IPR001732; UDPG_MGDP.
CC DR Pfam: PF00984; UDPG_MGDP_ch; 1.
CC DR SMART: SM00305; HincC; 1.
CC DR SMART: SM00306; HincN; 1.
CC KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
CC FT NP_BIND 2 19 NAD (POTENTIAL).
CC FT ACT_SITE 261 261 BY SIMILARITY.
CC SO SEQUENCE 895 AA; 102614 MW; B511AA68CCA41445 CRC64;
CC -----
CC
CC Query Match 52.9%; Score 37; DB 1; Length 895;
CC Best Local Similarity 75.0%; Pred. No. 33;
CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 6 KSFNRGEC 13
CC 1: 11111
CC Db 37 KALNRGEC 44
CC
CC RESULT 14
CC CHRL_BOMMO STANDARD; PRT; 177 AA.
CC ID CHRL_BOMMO
CC AC P1532;
CC DT 01-JAN-1990 (Rel. 13, Created)
CC DT 01-JAN-1990 (Rel. 13, Last sequence update)
CC DT 01-JAN-1990 (Rel. 13, Last annotation update)
CC DE CHORION PROTEIN ERB.1 PRECURSOR.
CC OS Bombyx mori (Silk moth).
CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
CC OC Bombycoidea; Bombycidae; Bombyx.
CC NX NCBI_TaxID=7091;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=88112521; PubMed=3338621;
CC RA Hibner B.L., Burke W.D., Iecanidou R., Rodakis G.C., Eickbush T.H.;
CC RT "Organization and expression of three genes from the silkworm early
CC RT chorion locus."
CC CC Dev. Biol. 125:423-431(1988).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
CC SILK MOTH.
CC -----
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RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF152371; AAD40242.1; -
 DR HSP: P01789; IMCP.
 DR InterPro: IPR003600; IG_Like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00406; IG_V.1.
 DR SMART: SM00410; IG_Like.1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1
 FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
 SQ
 Query Match 71.4%; Score 50; DB 11; Length 214;
 Best Local Similarity 61.5%; Pred. No. 0.091; 3; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SSPYTKSFNRGEC 13
 Db 202 TSPVTKCFNRREC 214
 RESULT 3
 ID 062019 PRELIMINARY; PRT; 548 AA.
 AC 062019;
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-AUG-1998 (TEMBLrel. 09, Last annotation update)
 DE B0462.1 PROTEIN.
 GN B0462.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Mortimore B.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Alincough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kersey J., Kirsten J., Laister N., Lathrell P.,
 RA Loughling J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
 RA Smalton R., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z81456; CAB03810.1;
 SQ SEQUENCE 548 AA; 63199 MW; 6B368C07E7ACAA13 CRC64;

QY 1 SSPYTKSFNRGEC 13
 Db 403 SGWLVKSIDRREC 415
 RESULT 4
 ID 09W008 PRELIMINARY; PRT; 1111 AA.
 AC 09W008;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE CG1141 PROTEIN.
 GN CG1141.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou X., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003475; AAF47652.1;
 DR HSP: P02640; IVIT.
 DR FlyBase: FBgn0035347; CG1141.
 DR InterPro: IPR001974; Gelsolin.
 DR InterPro: IPR003128; VHP.
 DR Pfam: PF00626; Gelsolin; 1.
 DR Pfam: PF02209; VHP; 1.
 DR PRINTS: PR00597; GELSOLIN.
 DR SMART: SM00262; GEL; 4.
 DR SMART: SM00153; VHP; 1.
 SQ SEQUENCE 1111 AA; 126001 MW; 186DD7B969E23B63 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 548;
 Best Local Similarity 61.5%; Pred. No. 20;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Query Match 57.1%; Score 40; DB 5; Length 1111;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PVTKSFNRGEC 13
DB 337 PVHTSLNRGDC 347

RESULT 5

09L17 PRELIMINARY; PRT; 821 AA.
AC 09L17;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CELLULOSE SYNTHASE-3 (FRAGMENT).
GN CESA-3.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Dhuga K.S., Helentjaris T.G.;
RT "Cellulose synthase-3 (Cesa-3) cDNA from maize";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF200527; AAF89963.1; -
FT NON_TER 1
SQ SEQUENCE 821 AA; 92900 MW; DB2AFE50807A0B0 CRC64;

Query Match 55.7%; Score 39; DB 10; Length 821;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SPVTKSFNRGEC 13
DB 806 SPYKALSRGQC 817

RESULT 6
09H550 PRELIMINARY; PRT; 74 AA.

AC 09H550;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BA207N4.1.3 (NOVEL PROTEIN (MUSC-H_263A.1 (TR:Q99993)) (ISOFORM 3))
DE (FRAGMENT).
GN BA207N4.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137143; CAC10455.1; -
FT NON_TER 74
SQ SEQUENCE 74 AA; 8503 MW; 999B9F5E0A0A0AF3 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 74;
Best Local Similarity 70.0%; Pred. No. 6.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVTKSFNRGEC 12
DB 59 PLTKSLRGCE 68

RESULT 7
09H551 PRELIMINARY; PRT; 108 AA.

AC 09H551;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BA207N4.1.1 (NOVEL PROTEIN (TRANSLATION OF CDNAS EM:U50534 AND EM:AL049784) (ISOFORM 1)) (FRAGMENT).
GN BA207N4.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL137143; CAC10454.1; -
FT NON_TER 108
SQ SEQUENCE 108 AA; 12060 MW; 8E3FCBF7FC599D41 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 108;
Best Local Similarity 70.0%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVTKSFNRGEC 12
DB 93 PLTKSLRGCE 102

RESULT 8
09RST9 PRELIMINARY; PRT; 258 AA.

AC 09RST9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMINOGLYCOSIDE N3'-ACETYLTRANSFERASE, TYPE IV.
GN DR2034.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; Pubmed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA McFalt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans RI.";
RL Science 286:1571-1577(1999).
DR EMBL; AE002040; AAF11584.1; -
DR TIGR; DR2034; -
DR InterPro; IPR003679; Antibiotic_NAT.
DR Pfam; PF02522; Antibiotic_NAT; 1.
SQ SEQUENCE 258 AA; 28432 MW; D2C3A5A4ADC3230 CRC64;

Query Match 54.3%; Score 38; DB 2; Length 258;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPVTKSFNR 10

Db 66 SSPVASFNR 75

RESULT 9

Q9US20 ID Q9US20 PRELIMINARY: PRT: 279 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
 GN SPAC181.02.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H-;
 RA McQuigall R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AL133361; CAB62428.1; -
 DR InterPro: IPR002123; Acyltransferase.
 DR Pfam: PF01553; Acyltransferase.1.
 KW Transferase; Acyltransferase.
 SQ SEQUENCE 279 AA; 31393 MM; E560D3366C9A0B63 CRC64;

Query Match 54.3%; Score 38; DB 3; Length 279;
 Best Local Similarity 70.0%; Pred. No. 25;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYTKSFNRGE 12
 Db 224 PPTKVFNRKE 233

RESULT 10

Q99993 ID Q99993 PRELIMINARY: PRT: 523 AA.
 AC Q99993;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE PAC CLONE 2G3A.
 GN WUSC.H.2G3A.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Favell T., Ritkin L., Tatch A., Le T.T.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC000062; AAB46343.1; -
 SQ SEQUENCE 523 AA; 60090 MM; 52B2A6ED285F0D43 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 523;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYTKSFNRGE 12
 Db 59 PLTKSLGRGE 68

RESULT 11

Q9T0J7 ID Q9T0J7 PRELIMINARY: PRT: 553 AA.
 AC Q9T0J7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE HYPOTHETICAL 61.2 KDA PROTEIN.
 GN T9A14.180 OR AT4G38900.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AL035656; CAB38624.1; -
 DR EMBL, AL161594; CAB80553.1; -
 DR InterPro: IPR001871; bZIP.
 DR Pfam: PF00170; bZIP.1.
 DR SMART: SM00338; BRIZ.1.
 KW Hypothetical protein.
 SQ SEQUENCE 553 AA; 61156 MM; 09F72DDCC63611F2 CRC64;

Query Match 54.3%; Score 38; DB 10; Length 553;
 Best Local Similarity 54.5%; Pred. No. 49;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYTKSFNRGEC 13
 Db 190 PLERSFSGEC 200

RESULT 12

Q9BXR6 ID Q9BXR6 PRELIMINARY: PRT: 569 AA.
 AC Q9BXR6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE COMPLEMENT FACTOR H-RELATED PROTEIN 5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11058592;
 RA McRae J.L., Cowan P.J., Power D.A., Mitchellhill K.I., Kemp B.E.,
 RA Morgan B.P., Murphy B.F.;
 RT "Human Factor H-related Protein 5 (FHR-5). A New Complement-Associated Protein."
 RL J. Biol. Chem. 276:6747-6754(2001).
 DR EMBL, AF295327; AAK15619.1; -
 SQ SEQUENCE 569 AA; 64419 MM; 7FAAE31707B0C112 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 569;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
|:| | |
Db 135 STPICSFTRGEC 147

RESULT 13

QY3N6 PRELIMINARY; PRT; 3012 AA.
ID QY3N6
AC QY3N6;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HYPOTHETICAL 338.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049784; CAB42442.1; -;
DR InterPro: IPR001745; GHMP_kinase.
DR PROSITE: PS00627; GHMP_KINASES_ATP; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 3012 AA; 338175 MW; 4034E2C82F74578F CRC64;

Query Match 54.3%; Score 38; DB 4; Length 3012;
Best Local Similarity 70.08%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVTKSFNRGE 12
|:| | |
Db 93 PLTKSLORGE 102

RESULT 14

ID 080307 PRELIMINARY; PRT; 67 AA.
AC 080307;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ORF23.
OS Bacteriophage 186.
OC viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OC P2-like viruses.
OX NCBI_TaxID=29252;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98371265; Pubmed=9705261;
RA Portelli R., Dodd I.B., Xue O., Egan J.B.;
RT "The late-expressed region of the temperate coliphage 186 genome.";
RL Virology 246:117-130(1998).
DR EMBL: U32222; AAC34153.1; -;
SQ SEQUENCE 67 AA; 7264 MW; 4995EFF98922D001 CRC64;

Query Match 52.9%; Score 37; DB 9; Length 67;
Best Local Similarity 66.78%; Pred. No. 9.3;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGE 12
|:| | | | |
Db 56 SSPVTKTINLME 67

RESULT 15

Q9UDK7 PRELIMINARY; PRT; 219 AA.
ID Q9UDK7
AC Q9UDK7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE PREGNANCY-ASSOCIATED PLASMA PROTEIN-A, PAPF-A (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93286045; Pubmed=7685339;
RA Oxvig G., Sand O., Kristensen T., Gleich G.J., Sottrup-Jensen L.;
RT "Circulating human pregnancy-associated plasma protein-A is disulfide-
bridged to the proform of eosinophil major basic protein.";
RL J. Biol. Chem. 268:12243-12246(1993).
FT NON_TER 1 1
FT NON_CONS 10 11
FT NON_CONS 35 36
FT NON_CONS 63 64
FT NON_CONS 76 77
FT NON_CONS 109 110
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FT NON_CONS 161 162
FT NON_CONS 167 168
FT NON_CONS 211 212
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 23562 MW; 6F0DE1EDA6E5BF94 CRC64;

Query Match 52.9%; Score 37; DB 4; Length 219;
Best Local Similarity 57.18%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 SPVTKSFN-RGEC 13
|:| | | | |
Db 30 SPVTKSFNFDGEC 43

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Job time: 327 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:43:51 ; Search time 1667.48 Seconds
(without alignments)
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Title: US-09-875-221A-115

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
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36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60.4	74.6	67	6	A97643	A97643 Sequence 10
2	35.2	43.5	1630	6	AX023367	AX023367 Sequence
3	34.2	42.2	202748	10	MMU0307670	AJ307670 Mus muscu
4	33.6	41.5	64	6	AX023342	AX023342 Sequence
5	33.4	41.2	96183	9	AL161896	AL161896 Human DNA
6	33.4	41.2	152053	2	AC022669	AC022669 Homo sapi
7	33	40.7	83599	8	AB005249	AB005249 Homo sapi
8	32.4	40.0	107526	9	HS111M5	284474 Human DNA s
9	32.4	39.8	57846	8	AP003053	AC0091273 Mus muscu
10	32.2	39.8	108930	2	AL513122	AP003053 Oryza sat
11	32.2	39.8	109422	2	AP003340	AL513122 Human DNA
12	32.2	39.8	150380	2	AP003792	AP003340 Oryza sat
13	32.2	39.8	207392	2	AC006558	AP003792 Oryza sat
14	32.2	39.5	5925	6	AX009712	AC006558 Homo sapi
15	32	39.5	95921	9	AC004141	AX009712 Sequence
16	32	39.5	158758	2	AC051635	AC004141 Homo sapi
17	32	39.5	187557	2	AC069032	AC051635 Homo sapi
18	32	39.5	209462	2	AC011814	AC069032 Homo sapi
19	32	39.3	321	9	HS294735	AC011814 Homo sapi
20	31.8	39.3	705	6	AR031183	AJ294735 Homo sapi
21	31.8	39.3	705	6	AR042588	AR031183 Sequence
22	31.8	39.3	705	6	AR052881	AR042588 Sequence
23	31.8	39.3	705	6	AR076259	AR052881 Sequence
24	31.8	39.3	705	6	AR080951	AR076259 Sequence
25	31.8	39.3	705	6	AR080951	AR080951 Sequence
26	31.8	39.3	708	6	AR042590	AX080951 Sequence
27	31.8	39.3	708	6	AR059283	AR042590 Sequence
28	31.8	39.3	708	6	AR076261	AR059283 Sequence
29	31.8	39.3	720	6	AR108864	AR076261 Sequence
30	31.8	39.3	6709	6	AX080952	AR108864 Sequence
31	31.8	39.3	7521	6	AX080951	AX080952 Sequence
32	31.8	39.3	8540	6	AR000006	AX080951 Sequence
33	31.8	39.3	8540	6	AR060919	AR000006 Sequence
34	31.8	39.3	8540	6	AR032413	AR060919 Sequence
35	31.8	39.3	8541	6	AR015960	AR032413 Sequence
36	31.8	39.3	9209	6	AR000007	AR015960 Sequence
37	31.8	39.3	9209	6	AR015961	AR000007 Sequence
38	31.8	39.3	9209	6	AR060920	AR015961 Sequence
39	31.8	39.3	9209	6	AX032414	AR060920 Sequence
40	31.8	39.3	18986	6	AR051652	AX032414 Sequence
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42	31.8	39.3	18986	6	HSAC000363	AR022290 Sequence
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ALIGNMENTS

RESULT 1
LOCUS A97643 67 bp DNA
DEFINITION Sequence 10 from Patent WO915549.
ACCESSION A97643
VERSION A97643.1 GI:6780935
KEYWORDS
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 67)
AUTHORS Humphreys,D.P.
TITLE Peptides
JOURNAL Patent: WO 9915549-A 10 01-APR-1999;
CELLTECH THERAPEUTICS LTD (GB); HUMPHREYS DAVID PAUL (GB)
FEATURES
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ORIGIN

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Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 gagctcacagtaacaaagcttaataagagagatgttgcagagagaaaaaatga 60
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Db 6 GAGCTCACAGTAACAAAGCTTAATAGAGAGAGCTGTGAGAGCAAAAAAATGA 65
Oy 61 ag 62
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Db 66 AG 67

RESULT 2

AX023367 1630 bp DNA PAT 15-SEP-2000
LOCUS Sequence 38 from Patent W0006605.
DEFINITION AX023367
ACCESSION AX023367.1 GI:10183779
VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Kufner, P., Zettl, F., Dreier, T., Baueuerle, P.A. and Borschert, K.
TITLE Heteromindodies
JOURNML Patent: WO 0006605-A 38 10-FEB-2000;
KUFNER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
BAUEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
BIOMEDIZINIS (DE)

FEATURES
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ORIGIN

Query Match 43.5%; Score 35.2; DB 6; Length 1630;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 3
MMU307670/c
LOCUS MMU307670 202748 bp DNA ROD 05-MAY-2001
DEFINITION Mus musculus St5 gene, L27a gene and Kiaa0298 gene.
ACCESSION AJ307670
VERSION AJ307670.1 GI:13992531
KEYWORDS KIAA0298 gene; L27a gene; ribosomal protein L27a; St5 gene gene;

SOURCE

Suppression of tumorigenicity 5.
house mouse.
Mus musculus

REFERENCE 1 (bases 1 to 202748)
AUTHORS Amid, C., Hankeln, T., Winterpacht, A., Zabel, B. and Schmidt, E.
JOURNML Unpublished
REFERENCE 2 (bases 1 to 202748)
AUTHORS Hankeln, T.
TITLE Direct Submission
JOURNML Submitted (04-MAY-2001) Hankeln T., Inst. Molekulargenet., Univ.
Mainz, Becherweg 32, D-55099 Mainz, GERMANY
FEATURES
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HYDFECLTCLSVROLTRIPASLLERRVFVADKLTSSCGSHAVVALLYPPSWHT
FIYVLPASMDIYCCPTPLVGLSSSLPLKLEIPEEALMVNLGDSRFETROMDEDT
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[illegible]

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REFERENCE 1 (bases 1 to 64)
AUTHORS Kufner,P., Zettl,F., Dreier,T., Baenerle,P.A. and Borschert,K.
TITLE Heteromimibodies
JOURNAL Patent: WO 0006605-A 13 10-FEB-2000;
KUFNER PETER (DE) ; ZETTL FLORIAN (DE) ;
BAENERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
BIOMEDIZINIS (DE)
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/db_xref="taxon:32630"
/note="synthetic, no natural origin"
BASE COUNT 15 a 15 c 22 g 12 t
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Best Local Similarity 81.2%; Pred. No. 30;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 4 GAGCTCGCCCGTCACAAAGAGCTTCAACAGGAGAGAGTGTGAGGTGG 51
RESULT 5
AL161896/c AL161896 96183 bp DNA PRI 20-JAN-2001
LOCUS Human DNA sequence from clone RP11-261P24 on chromosome 13,
DEFINITION complete sequence.
ACCESSION AL161896
VERSION AL161896.16 GI:12330752
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 96183)
REFERENCE 1
AUTHORS Phillimore,B.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jan 22, 2001 this sequence version replaced gi:12329254.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-261P24 is from the library RPCI-11.1 constructed by the group
of Pister de Jong. For further details see
http://www.choi.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-261P24. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-261P24 is at 96183 in this
sequence. The true left end of clone RP11-31K22 is at 59428 in this

sequence. The true right end of clone RP11-573N10 is at 100 in this
sequence.
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repeat_region repeat: matches 1. .75 of consensus"
3518. .3834
/note="L1MB8 repeat: matches 5837. .6173 of consensus"
5528. .5599
/note="12 copies 6 mer tattta 69% conserved"
5533. .5604
/note="36 copies 2 mer at 69% conserved"
5766. .6068
/note="AluB repeat: matches 7. .303 of consensus"
6949. .7264
/note="AluB repeat: matches 1. .307 of consensus"
7380. .7501
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8192. .8407
/note="L2 repeat: matches 2064. .2289 of consensus"
8475. .8506
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8929. .9103
/note="MER3 repeat: matches 4. .171 of consensus"
9104. .9421
/note="AluB repeat: matches 1. .306 of consensus"
9422. .9450
/note="MER3 repeat: matches 171. .216 of consensus"
9491. .9595
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9596. .9909
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9910. .9997
/note="MER3 repeat: matches 225. .319 of consensus"
11665. .11763
/note="MIR repeat: matches 47. .149 of consensus"
11991. .12022
/note="8 copies 4 mer tgtg 90% conserved"
12274. .12568
/note="AluX repeat: matches 20. .311 of consensus"
12577. .12879
/note="Alu repeat: matches 1. .304 of consensus"
13406. .13549
/note="MIR repeat: matches 1. .146 of consensus"
13554. .13585
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13682. .13715
/note="17 copies 2 mer ac 97% conserved"
13684. .13715
/note="8 copies 4 mer acac 100% conserved"
13752. .13779
/note="14 copies 2 mer ca 96% conserved"
13784. .14048
/note="MIR repeat: matches 189. .465 of consensus"
14716. .15018
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15567. .15842
/note="AluB repeat: matches 3. .305 of consensus"
16752. .16916
/note="MIR repeat: matches 63. .227 of consensus"
17700. .17838
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18111. .18314
/note="MIR repeat: matches 157. .359 of consensus"
18317. .18428
/note="28 copies 4 mer ctcc 71% conserved"

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repeat_region      18800..18956
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repeat_region      19780..20069
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repeat_region      38553..39205
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repeat_region      39561..39944
                    /note="MST1 repeat: matches 1..426 of consensus"
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repeat_region      42330..42393

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                    42692..42857
repeat_region      /note="L1MC2 repeat: matches 5654..5816 of consensus"
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repeat_region      /note="AluSg repeat: matches 1..293 of consensus"
                    43152..43183
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                    43184..43479

Query Match      41.2% Score 33.4; DB 9; Length 96183;
Best Local Similarity 68.7%; Pred. No. 46;
Matches 46; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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QY      2 agccaccagtaacaaaagcttaataagagagagtggtgagaggaacaaatgaa 61
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Db      29011 AGATCTGCATGAGTAATATCTCCGTCTGGAAACTGTGAAGAAAGAAATTTAA 28952
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Db      28951 TAAATCT 28945

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RESULT      6
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LOCUS      Homo sapiens chromosome 15 clone RP11-96B23 map 15, WORKING DRAFT
DEFINITION
ACCESSION
VERSION      AC022669.4 GI:9966291
KEYWORDS
SOURCE      HNG: HTGS_PHASE1; HTGS_DRAFT.
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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REFERENCE
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Binkley,C., Beda,F.,
              Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
              Choquel,Y., Colangelo,M., Collins,S., Collins,A., Cooke,P.,
              Dearlano,K., Dewar,K., Domino,M., Doyle,M., Fenebor,J.,
              Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
              Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
              Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
              Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,
              Macdonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K.,
              McPheters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
              Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
              Pierre,N., Pisanil,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
              Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
              Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
              Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
              Zimmer,A. and Zody,M.

```

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TITLE      Direct Submission
JOURNAL
COMMENT      Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
              Research, 320 Charles Street, Cambridge, MA 02141, USA
              On Sep 4, 2000 this sequence version replaced gi:7229803.
              All repeats were identified using RepeatMasker:
              Smit, A.F.A. & Green, P. (1996-1997)
              http://ftp.genome.washington.edu/RM/RepeatMasker.html
              ----- Genome Center
              Center: Whitehead Institute/ MIT Center for Genome Research
              Center code: WIRB
              Web site: http://www-seq.wi.mit.edu
              Contact: sequence_submissions@genome.wi.mit.edu
              ----- Project Information
              Center project name: L4938
              Center clone name: 96-B-23
              ----- Summary Statistics
              Sequencing vector: M13; M7815; 93% of reads

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Sequencing vector: Plasmid: n/a; %0.f%% of reads
7.39091718610864Chemistry: Dye-terminator Big Dye; 100% of
reads
Assembly program: Phrap; version 0.960731
Consensus quality: 136451 bases at least Q40
Consensus quality: 143612 bases at least Q30
Consensus quality: 146365 bases at least Q20
Insert size: 158000; agarose-fp
Insert size: 148853; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality cov.
NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
785 884: gap of 100 bp
885 1956: contig of 1072 bp in length
1957 2056: gap of 100 bp
2057 3113: contig of 1057 bp in length
3114 3213: gap of 100 bp
3214 4817: contig of 1604 bp in length
4818 4917: gap of 100 bp
4918 6582: contig of 1665 bp in length
6583 8059: contig of 1377 bp in length
8060 8159: gap of 100 bp
8160 22369: contig of 14210 bp in length
22370 22469: gap of 100 bp
22470 24974: contig of 2505 bp in length
24975 25074: gap of 100 bp
25075 27206: contig of 2132 bp in length
27207 27306: gap of 100 bp
27307 29420: contig of 2114 bp in length
29421 29520: gap of 100 bp
29521 32000: contig of 2480 bp in length
32001 32100: gap of 100 bp
32101 36330: contig of 4230 bp in length
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36431 39067: contig of 2637 bp in length
39068 39167: gap of 100 bp
39168 42564: contig of 3397 bp in length
42565 42664: gap of 100 bp
42665 46664: contig of 4000 bp in length
46665 46764: gap of 100 bp
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55270 55369: gap of 100 bp
55370 58831: contig of 3462 bp in length
58832 58931: gap of 100 bp
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64078 64177: gap of 100 bp
64178 68808: contig of 4631 bp in length
68809 68908: gap of 100 bp
68909 74170: contig of 5262 bp in length
74171 74270: gap of 100 bp
74271 79296: contig of 5026 bp in length
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79397 84724: contig of 5328 bp in length
84725 84824: gap of 100 bp
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94722 94821: gap of 100 bp
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100197 100296: gap of 100 bp
100297 107015: contig of 6719 bp in length
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FEATURES
source
107116 114507: contig of 7392 bp in length
* 114508 114607: gap of 100 bp
* 114608 122671: contig of 8064 bp in length
* 122672 122771: gap of 100 bp
* 122772 128052: contig of 5281 bp in length
* 128053 128152: gap of 100 bp
* 128153 138583: contig of 10431 bp in length
* 138584 138683: gap of 100 bp
* 138684 150248: contig of 11565 bp in length
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74271..79296
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79397..84724
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84825..89713
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94822..100196
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misc_feature	107116..114507	/note="assembly_fragment"
misc_feature	114608..122671	
Query Match	41.2% Score 33.4; DB 2; Length 152053;	
Best Local Similarity	68.7% Pred. No. 47; Mismatches 21; Indels 0; Gaps 0;	
Matches	46; Conservative 0; Mismatches 0; Gaps 0;	
2	agctaccagtaacaaagcttaataagagagagtgctgagagagaaataatgaa 61	
54458	AGATCTGACGATGAACAATTAATCTTCGCTCGGAAACGTGTAAGAGAAAGCAATTTAA 54517	
62	gaaact 68	
54518	TAAATACT 54524	
RESULT 7		
AB005249/c	AB005249 83599 bp DNA PLN 27-DEC-2000	
LOCUS	Arabidopsis thaliana genomic DNA, chromosome 5, pl clone:MXM12.	
DEFINITION	AB005249 BA000015	
ACCESSION	AB005249.1 GI:2264321	
VERSION		
KEYWORDS		
SOURCE	Arabidopsis thaliana (strain:Columbia) DNA, clone:lib:Mitsui P1 clone:MXM12.	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (sites)	
AUTHORS	Sato,S., Kocani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M., Miyajima,N. and Tabata,S.	
TITLE	Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones	
JOURNAL	DNA Res. 4 (3), 215-230 (1997)	
MEDLINE	97471969	
REFERENCE	2 (bases 1 to 83599)	
AUTHORS	Nakamura,Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)	
COMMENT	Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MXM12 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGEN (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/Netgene/) and SplicePredictor (Volker Brendel, Stanford University, http://gremliini.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MBK20. Location/Qualifiers 1. 83599 /organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702" /chromosome="5"	
FEATURES		
source		

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VHLVGHQDNPAVLPMPKRVVLSYKMLQHLRTMLLEEMALLIVDESHLRCSKRS
DPPEIKTVLDVAEKVYKIIILSGTPSVSRPOLLDKDEKFEKTCCEGVILVGIQKIF
ODFSKGTLLLELINTLNOTVMIRLQKHLTPPKRQIOTVILTKRKDIDIMAAIVS
EAKKOGDAIEVEEKESHEPDONARGSNEACHVAENSDGNSKENDLCKLSKLOOL
GIATLSAREWLSLAPILSLGDIYPTPEIDGROSSKRWVFPAMHHKVEITGLOFTCDK
IGFVRIDCTTLPBRODLAVOSFORSSEKAIITIGEAGVGLDPSAONVFELEPKT
PSLLQADRAHRRGQTSANVYIFCADIYDESMWMLNKLHRIISTDTGKYDKGT
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EKNEPSTDDPVHUALIEFKMKSLRPIKRLKGLDPLPLSELSYLSSESTSH
SEGILRGSKRRNTPFETSLPBNVAVITVNLRSQHOKKEKETQAMWSNEPLK
LCQKPCAGYNKKEPEYLEDCELCACYEDYRTKTSRYIROIEHICITNCKLDHOLV
KRLRPLERKRTYINKAPLPELFAKRLVNDPTGNAHADHIIIPVQGGECR
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/evidence=not_experimental
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/db_xref="GI:10176716"
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KTSPPSVSVRYVKTNILVYNKASRISQNSPEDLSKLNKEKGIIVPVKCDY
LEKTDLEKVKVSRISENKKSEDTLKNKEKAKIDEPVPCDVLKTSIDAKVRISE
NKNEERIKKRLKNKEKNTIDEPVRPDADVKTLYVSSVEKKKKKKSTSVKISFT
QOSEKKTIRSTGKSSLSLSPRPSPSVYTGSPRPRTOTSSKISLPRKQSGSA
NLVTPKPEKIRKIRIGLKVTPPPPKQDMNRKGVLEPKEDSTTISIRKRTV
VOEKLRTSDVNRKKSLLKDKRECVKINGEGKREKVVLRKRRKVEKKILNNVNI
EEYNNKLEEVKSKSVKALVGAFFETVSLQDNMTSOKKKIOSKSTSSQVAGC"
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28500..28883)
/note="contains similarity to heparanase
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DLIYKIVINKVYKNSWLHKPILVAPGPFYQOMYTKLLETSGSVVDVYVHTYNG
SGNDPALYKRTIMPSYLSQVSKTRFDVNOTIQDEGPNASPRVSGGAYNSGRHVD
TFIDSEWTLDDGSHSAHNRKVCYKOTLVGGFVGLERGTVPNDYISALLHRLK
KGLVAVQTDKPPQLRVYAHCSGRAGVTLILINSQSDFTVSVNGINVLNLSRK
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Query Match
Best Local Similarity 40.7%; Score 33; DB 8; Length 83599;
Matches 45; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 3 gctccaccgtacaagaagcttaatagagagagtgtagaggaagaadaaatgaag 62
Db 6199 GTTTAAAGAAAAACCACTTAACACAGCAATGTTGATTCACAAAAAAGAAAG 6140
QY 63 aaac 67
Db 6139 AAAC 6135

RESULT 8
LOCUS HS11M5 107526 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from PAC 11M5 on chromosome 6. Contains BBCT1,
RFP finger protein, EST, STS, tRNAs and polymorphic repeat.
ACCESSION Z84474
VERSION Z84474.1 GI:1903188
KEYWORDS 6p21.3; BBCT1; repeat polymorphism; RFP transforming protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 107526)
Nidlett,D.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1997) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, UK. Chromosome 6 Project Group
(http://www.sanger.ac.uk/chr6/); E-mail enquiries:
hunquyer@sanger.ac.uk
COMMENT
On Mar 21, 1997 this sequence version replaced g1:1806002.
de Jong P.J., enquires: http://bbccp.med.buffalo.edu/ IMPORTANT:
This sequence is the entire insert of clone 11M5. This sequence
has been finished according to sequence map criteria as follows.
An attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 11M5 is at 1 in this sequence. The true
right end of clone 11M5 is at 107526.
11M5 is from the human PAC library described in Ioannou A.P. et al
Nature Genet 6, 84-89.

FEATURES
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/chromosome="6"
/map="6p21.3"
/clone_lib="RPC1-1"
/clone="RP1-11M5"
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941..1225
/note="Alusx repeat: matches 2..299 of consensus"
1264..1376
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incomplete repeat"
1648..1929
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/note="Ala-tRNA"
5042..5329
/note="Alusx repeat: matches 1..294 of consensus"
5332..5581
/note="MER42c repeat: matches 178..432 of consensus"
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trna
repeat_region
repeat_region
repeat_region

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12043. .12329
repeat_region /note="AluSx repeat: matches 292. .6 of consensus"
12348. .12448
/note="MER33 repeat: matches 203. .313 of consensus"
12843. .13179
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repeat_region /note="AluSg repeat: matches 1. .300 of consensus"
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14370. .14661
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20623. .20754
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21340. .21363
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21927. .22031
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32962. .33152
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34146. .34226
repeat_region /note="L1MD2 repeat: matches 479. .570 of consensus"
34270. .34433
repeat_region /note="MER34 repeat: matches 181. .14 of consensus"
34694. .34996
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36165. .36455
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37879. .38207
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38254. .38510
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39624. .39914
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40588. .42050
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42051. .42350
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42352. .46319
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Query Match	40.0%	Score 32.4	DB 9	Length 107526
Best Local Similarity	68.2%	Pred. No. 83		
Matches 45	Conservative 0	Mismatches 21	Indels 0	Gaps 0

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Db	17162	CAGAAACGCTTTGGAAGTTGACGCTATAGAGAAAGAAAAAAGGAAAGTGTATGTG 17221
Oy	75	gcaact 80
Db	17222	GAAATT 17227

RESULT 9	AC091273/C	LOCUS	DEFINITION
AC091273	216383 bp	DNA	HTG 13-JUN-2001
Mus musculus	clone RP23-78F6	WORKING DRAFT	SEQUENCE, 5 unordered

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AC091273	AC091273.2	GI:14389358	HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	house mouse.
Mus musculus	clone RP23-78F6			

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

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2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
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2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
2	(bases 1 to 216383)			
Unpublished				

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	Barren,B., Linton,L., Nusbaum,C. and Lander,E.	Mammalia: Euthera		

[illegible]

misc_feature	join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" /note="Pseudogene, similar to Arabidopsis thaliana chr 1, FIK323.13" /pseudo join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" /note="hypothetical protein" /codon_start=1 /protein_id="BAB55687.1" /db_xref="GI:14164434" /translation="MSNEKVPNSNAP1AEOGNAPONGSKNHKPGASSEETWTPSPDPFPMETIOVAPRRDDPDYIRIEQAVNRKSRKACGNRPEQVEMPTASAPRPTST SAGSGGKKRRGEBRSKNKLPKETYINVALDDQSKLEPIYVRKESNACGTLVTRCPINVKLTWEYVDNHIKITLWNLQAKYEFVPGSEYRGVADLAKKGDWRPKWSOLNDYVQNKLPFTFDGHIISQADWDTEYADRTTEALALRRKMSALAKKNYPHRLGSSGAGHVDQREIEKORFAAGKPLLVDPWVERSNWVARSTGQSEGDILFETPDIEEYTN LQOITYEKRSOEFVRRERDDOTALGAEHSGVRGSLSKSMVGFPODAPSYKRR DTEYKQSLDYIAOVKEHPSYSLAENPAPLPPDSOOPQOSAOQNTNVSAGVSKR TSTPRVDSITGPTKCSIVYPIGRAGKTEVANGALIPGRQFINNTAIPDYAVOVAKY HSDVSLDLIPABGILLDGAVNQFTLMHRDITLSAAYLAAGSSTPSSQATTA AAPASPEPPSPRHPPSPRPRLRSPRPPTPPPSQOPLPTPDVVASPTSPKHQ AAPAPSPVOTSPPTQOSALVEVHLPDQTSBPKSNTLEPRKIIPKLISTYDAPKIDKKEFMFAPFNSEKRRKLAVHLSDSOKSVAPLAODEVOSMSADVPETVEKPLPPT YLMNKLPMEMVHEMWYKASRKGLGFSVAVPECTFMSGPCIGIFIFISFDLYALYKL			
gene	join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" /note="Pseudogene, similar to Arabidopsis thaliana chr 1, FIK323.13" /pseudo join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" /note="hypothetical protein" /codon_start=1 /protein_id="BAB55687.1" /db_xref="GI:14164434" /translation="MSNEKVPNSNAP1AEOGNAPONGSKNHKPGASSEETWTPSPDPFPMETIOVAPRRDDPDYIRIEQAVNRKSRKACGNRPEQVEMPTASAPRPTST SAGSGGKKRRGEBRSKNKLPKETYINVALDDQSKLEPIYVRKESNACGTLVTRCPINVKLTWEYVDNHIKITLWNLQAKYEFVPGSEYRGVADLAKKGDWRPKWSOLNDYVQNKLPFTFDGHIISQADWDTEYADRTTEALALRRKMSALAKKNYPHRLGSSGAGHVDQREIEKORFAAGKPLLVDPWVERSNWVARSTGQSEGDILFETPDIEEYTN LQOITYEKRSOEFVRRERDDOTALGAEHSGVRGSLSKSMVGFPODAPSYKRR DTEYKQSLDYIAOVKEHPSYSLAENPAPLPPDSOOPQOSAOQNTNVSAGVSKR TSTPRVDSITGPTKCSIVYPIGRAGKTEVANGALIPGRQFINNTAIPDYAVOVAKY HSDVSLDLIPABGILLDGAVNQFTLMHRDITLSAAYLAAGSSTPSSQATTA AAPASPEPPSPRHPPSPRPRLRSPRPPTPPPSQOPLPTPDVVASPTSPKHQ AAPAPSPVOTSPPTQOSALVEVHLPDQTSBPKSNTLEPRKIIPKLISTYDAPKIDKKEFMFAPFNSEKRRKLAVHLSDSOKSVAPLAODEVOSMSADVPETVEKPLPPT YLMNKLPMEMVHEMWYKASRKGLGFSVAVPECTFMSGPCIGIFIFISFDLYALYKL			
gene	join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" /note="Pseudogene, similar to Arabidopsis thaliana chr 1, FIK323.13" /pseudo join(132952..33246,33357..33575,34794..34933,35040..35316,35822..36089,37783..37846,37866..37986,38087..38266,40617..40765,40866..41143,41482..41695,42291..42624) /gene="P0047B08.10" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" complement(join(42811..43002,43277..43358,43639..43890,43976..46209,46300..46497)) /gene="P0047B08.11" /note="hypothetical protein" /codon_start=1 /protein_id="BAB55687.1" /db_xref="GI:14164434" /translation="MSNEKVPNSNAP1AEOGNAPONGSKNHKPGASSEETWTPSPDPFPMETIOVAPRRDDPDYIRIEQAVNRKSRKACGNRPEQVEMPTASAPRPTST SAGSGGKKRRGEBRSKNKLPKETYINVALDDQSKLEPIYVRKESNACGTLVTRCPINVKLTWEYVDNHIKITLWNLQAKYEFVPGSEYRGVADLAKKGDWRPKWSOLNDYVQNKLPFTFDGHIISQADWDTEYADRTTEALALRRKMSALAKKNYPHRLGSSGAGHVDQREIEKORFAAGKPLLVDPWVERSNWVARSTGQSEGDILFETPDIEEYTN LQOITYEKRSOEFVRRERDDOTALGAEHSGVRGSLSKSMVGFPODAPSYKRR DTEYKQSLDYIAOVKEHPSYSLAENPAPLPPDSOOPQOSAOQNTNVSAGVSKR TSTPRVDSITGPTKCSIVYPIGRAGKTEVANGALIPGRQFINNTAIPDYAVOVAKY HSDVSLDLIPABGILLDGAVNQFTLMHRDITLSAAYLAAGSSTPSSQATTA AAPASPEPPSPRHPPSPRPRLRSPRPPTPPPSQOPLPTPDVVASPTSPKHQ AAPAPSPVOTSPPTQOSALVEVHLPDQTSBPKSNTLEPRKIIPKLISTYDAPKIDKKEFMFAPFNSEKRRKLAVHLSDSOKSVAPLAODEVOSMSADVPETVEKPLPPT YLMNKLPMEMVHEMWYKASRKGLGFSVAVPECTFMSGPCIGIFIFISFDLYALYKL			
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Query Match	39.8%	Score 32.2	DB 8	Length 57846
Best Local Similarity	63.6%	Pred. No. 91		
Matches 49	Conservative 0	Mismatches 28	Indels 0	Gaps 0
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Db 33840	ctcagagaagcagcaggaagcgtggcggtgcctagaaagtgaaaggaagaaaaaagcagaaa 33899			
OY 64	aaacgcctatagcaatt 80			
Db 33900	agctatgcctatagcatttt 33916			
RESULT 11				
AL513122/c				
LOCUS	AL513122	108930 bp	DNA	PRI 26-JUN-2001
DEFINITION	Human DNA sequence from clone RP11-477J21 on chromosome 9, complete sequence.			
ACCESSION	AL513122			
VERSION	AL513122.7	GI:14572568		
KEYWORDS	HTG.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Laird,G.			
TITLE	Direct Submision			
JOURNAL	Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk			

COMMENT	REQUESTS: clonerequests@sanger.ac.uk	REPLACED: gi:14270608.
On Jun 27, 2001 this sequence version replaced gi:14270608.		
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.		
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em', EMBL, SW', SWISSPROT; Tr', TREMBL; Wp', WORMPEP; information on the WORMPEP database can be found at		
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone configs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at		
http://www.sanger.ac.uk/HGP/Chr9		
RP11-477J21 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see		
http://www.choil.org/bacpac/home.htm		
VECTOR: PBAC93.6		
IMPORTANT: This sequence is not the entire insert of clone RP11-477J21. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.		
The true right end of clone RP11-477J21 is at 108930 in this sequence. The true left end of clone RP11-424J3 is at 23985 in this sequence. The true right end of clone RP11-165P4 is at 100 in this sequence.		
FEATURES		
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	/chromosome="9"	
	/clone="RP11-477J21"	
	/clone_1lb="RPC1-11.2"	
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	605..725	
repeat_region	/note="L2 repeat: matches 2624. .2746 of consensus"	
	879..1178	
repeat_region	/note="AluJb repeat: matches 1. .309 of consensus"	
	1187..1672	
repeat_region	/note="L1MC4 repeat: matches 7492. .7975 of consensus"	
	1673..1972	
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	1973..2675	
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	3053..3202	
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	4252..4523	
repeat_region	/note="AluSg repeat: matches 1. .283 of consensus"	
	4641..4753	
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	5008..5134	
repeat_region	/note="L1MB1 repeat: matches 6042. .6168 of consensus"	
	5296..5413	
repeat_region	/note="HERVL repeat: matches 4908. .5022 of consensus"	
	5414..5637	
repeat_region	/note="M17G repeat: matches 1. .216 of consensus"	
	5638..5940	
repeat_region	/note="AluSg repeat: matches 1. .302 of consensus"	
	5941..6209	
repeat_region	/note="M17G repeat: matches 216. .510 of consensus"	
	6210..6327	
repeat_region	/note="HERVL repeat: matches 4794. .4908 of consensus"	
	6328..6781	

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/note="MLT1J repeat: matches 1. .516 of consensus"
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repeat_region
/note="HRRV3 repeat: matches 4402. .4794 of consensus"
7157. .7314
repeat_region
/note="FRAM repeat: matches 1. .158 of consensus"
8178. .8363
repeat_region
/note="MLT1J repeat: matches 1. .200 of consensus"
8396. .8634
repeat_region
/note="MLT1C repeat: matches 220. .466 of consensus"
8664. .8966
repeat_region
/note="AluSg repeat: matches 1. .308 of consensus"
9734. .10026
repeat_region
/note="Aluub repeat: matches 1. .304 of consensus"
10611. .11123
repeat_region
/note="MLT2B repeat: matches 1. .448 of consensus"
12545. .12786
repeat_region
/note="MLT1C repeat: matches 1. .229 of consensus"
13425. .13855
repeat_region
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13905. .14075
repeat_region
/note="MIR repeat: matches 50. .216 of consensus"
14560. .14653
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15446. .15938
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16000. .16056
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18400. .18716
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repeat_region
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repeat_region
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23007. .23286
repeat_region
/note="AluSg repeat: matches 5. .283 of consensus"
23327. .23364
repeat_region
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23383. .23579
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23639. .23950
repeat_region
/note="AluSx repeat: matches 1. .298 of consensus"
24131. .24437
repeat_region
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repeat_region
/note="L2 repeat: matches 2698. .2747 of consensus"
24643. .24880
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24954. .25299
repeat_region
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25300. .25344
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/note="L2 repeat: matches 2197. .2235 of consensus"
25345. .25707
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25708. .25752
repeat_region
/note="L2 repeat: matches 2151. .2197 of consensus"
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repeat_region
/note="AluY repeat: matches 1. .309 of consensus"
27703. .27989
repeat_region
/note="Aluub repeat: matches 1. .295 of consensus"

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/note="MIR repeat: matches 12. .262 of consensus"
repeat_region 29964. .30044
/note="MIR repeat: matches 127. .197 of consensus"
repeat_region 30045. .30356
/note="AluSx repeat: matches 3. .312 of consensus"
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/note="MIR repeat: matches 92. .127 of consensus"
repeat_region 30668. .30932
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repeat_region 31360. .31519
/note="L2 repeat: matches 2540. .2710 of consensus"
repeat_region 31530. .31778
/note="L2 repeat: matches 2483. .2746 of consensus"
repeat_region 31834. .32101
/note="L2 repeat: matches 2243. .2508 of consensus"
repeat_region 33093. .33156
/note="MIR repeat: matches 86. .151 of consensus"
repeat_region 33878. .34052
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repeat_region 34281. .34362
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repeat_region 35373. .35551
/note="L2 repeat: matches 2520. .2710 of consensus"
repeat_region 35560. .35847
/note="MER63B repeat: matches 1. .278 of consensus"
repeat_region 35848. .36062
/note="THE1C repeat: matches 166. .371 of consensus"
repeat_region 36063. .36363

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Query Match 39.8%; Score 32.2; DB 9; Length 108930;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 46; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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QY 12 taacaaaagcttaatagaggagagtgctgaggaagaaaaaatgaagaactgcgt 71
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Db 9499 TGACTAAATCATTAATAGAGTGTCTTGCGGTACACAAAGAAAGAAACTT 9440

QY 72 atagcaatt 80
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Db 9439 ATAGCAATT 9431

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RESULT 12
 AP003340
 LOCUS Oryza sativa chromosome 1 clone OJ1316_H05, *** SEQUENCING IN
 DEFINITION PROGRESS ***, in ordered pieces.
 ACCESSION AP003340
 VERSION AP003340.1 GI:13359076
 KEYWORDS HTG: HTGS PHASE2
 SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1316_H05.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (sites)
 REFERENCES
 Sasaki,T., Matsumoto,T. and Yamamoto,K.
 Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, BAC
 clone:OJ1316_H05
 Published Only in DataBase (2001) In press
 JOURNAL 2 (bases 1 to 109422)
 REFERENCE
 Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE	COMMENT	FEATURES	BASE COUNT	ORIGIN
<p>TITLE Direct Submission</p> <p>JOURNAL Submitted (28-FEB-2001) Takui Sasaki, National Institute of Agricultural Resources, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan</p> <p>(E-mail:tsasaki@bar.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)</p> <p>The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.</p> <p>NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.</p> <p>* NOTE: This is a 'working draft' sequence.</p> <p>* This sequence will be replaced</p> <p>* by the finished sequence as soon as it is available and</p> <p>* the accession number will be preserved.</p> <p>Location/Qualifiers</p> <p>1. 109422</p> <p>/organism="Oryza sativa"</p> <p>/cultivar="Nipponbare"</p> <p>/db_xref="taxon:4530"</p> <p>/chromosome="1"</p> <p>/clone="OJ131_H05"</p>	<p>30559 a 23093 c 23374 g 32146 t 250 others</p>	<p>Query Match 39.8%; Score 32.2; DB 2; Length 109422;</p> <p>Best Local Similarity 63.6%; Pred. No. 94;</p> <p>Matches 49; Conservativity 0; Mismatches 26; Indels 0; Gaps 0;</p>	<p>Oy 4 ctccaccagtaaaaaaactttaaataagagagatgcttgaagagaaaaaataatgaaga 63</p> <p>DB 102204 CTCAGACAGCATGGAAGGAGGAGGAGTGGCTAGAAAGTTGAGAGAAAAAAGGANA 102263</p> <p>Oy 64 aaacgtctatgacatt 80</p> <p>DB 102264 AGTATGCTATGACATTT 102280</p>	<p>RESULT 13</p> <p>LOCUS AP003792/c</p> <p>DEFINITION Oryza sativa chromosome 1 clone OJ1159-D09, *** SEQUENCING IN PROGRESS ***, In ordered pieces.</p> <p>ACCESSION AP003792</p> <p>VERSION AP003792.1 GI:14572677</p> <p>KEYWORDS HTG: HTGS, PHASE2.</p> <p>SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1159-D09.</p> <p>ORGANISM Oryza sativa</p> <p>REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.</p> <p>1 (sites)</p> <p>Sasaki,T., Matsumoto,T. and Yamamoto,K.</p> <p>Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OJ1159-D09</p> <p>Published Only in Database (2001) In press</p> <p>2 (bases 1 to 150380)</p> <p>Sasaki,T., Matsumoto,T. and Yamamoto,K.</p> <p>Direct Submission</p> <p>Submitted (27-JUN-2001) Takui Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan</p> <p>(E-mail:tsasaki@bar.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)</p> <p>The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.</p> <p>NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them</p>

are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. 150380

/organism="Oryza sativa"

/cultivar="Nipponbare"

/db_xref="taxon:4530"

/chromosome="1"

/clone="OJ1159_D09"

BASE COUNT 41983 a 33202 c 32862 g 42033 t 300 others

ORIGIN

Query Match 39.8%; Score 32.2; DB 2; Length 150380; +

Best Local Similarity 63.6%; Pred. No. 95;

Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 ctgcacgtaacaaaagctttaagaggagtggtgagagagaaaaaatgtaaga 63

Db 145440 CTCAGAAACACTGAGAGGTGGAGCTTGCTCGAAGATTGAAGAAAAAAGGAAA 145381

QY 64 aaactgcctatagcaatt 80

Db 145380 AGTATGCTATAGCATTT 145364

RESULT 14

AC006558/c DNA HTG 10-FEB-1999

LOCUS

DEFINITION Homo sapiens chromosome 9 clone hRPK.477_J_21 map 9, *** SEQUENCING

IN PROGRESS ***, 7 unordered pieces.

AC006558

AC006558.1 GI:4262259

HTG: HTGS_PHASE1.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 207392)

Bliren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 9, clone hRPK.477_J_21

Unpublished

2 (bases 1 to 207392)

Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baker,J., Baldwin,J., Barua,N., Beckerly,R., Benn,J., Brown,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., Dearellano,K., Depuyre,E., Devon,K., Dewar,K.,

Donelan,J., Doyle,M., Ferrelira,P., Fitzhugh,W., Forrest,C.,

Funkel,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,

Karas,A., Leaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,

Marguis,N., McKean,P., McGurk,A., McKernan,K., McLaughlin,J.,

Meidrum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,

Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,

Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,

Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.

Direct Submission

Submitted (10-FEB-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: Smit, A.F.A. &

Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:49:56 ; Search time 230.28 Seconds
(without alignments)
301.560 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 81

Sequence: 1 gagctccaccgtaacacaaa.....gaaacgtctatgcaatg 81

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq.1101:*
1: /SIDSR/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDSR/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDSR/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDSR/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDSR/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDSR/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDSR/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDSR/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDSR/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDSR/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDSR/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDSR/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDSR/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDSR/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDSR/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDSR/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDSR/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDSR/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDSR/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDSR/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDSR/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDSR/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.2	63.2	66	20	AAK55755
2	35.2	43.5	1630	21	AAZ50588
3	33.6	41.5	64	21	AAZ50601
4	32.8	40.5	548	16	AAZ23297
5	32	39.5	4691	16	AAO92546
6	32	39.5	5924	21	AAZ38921
7	32	39.5	5925	21	AAZ38770
8	32	39.5	6166	16	AAO92547
9	31.8	39.3	705	18	AAZ61240
10	31.8	39.3	708	18	AAZ61242
11	31.8	39.3	708	21	AAA63530

12	31.8	39.3	720	18	AAZ62511	Primate anti-hu
13	31.8	39.3	720	19	AAV35486	Macaque primatized
14	31.8	39.3	725	20	AAZ22287	Nucleotide sequenc
15	31.8	39.3	6709	22	AAZ30339	Bicistronic plasmid
16	31.8	39.3	7521	22	AAZ30315	Bicistronic chimera
17	31.8	39.3	8540	15	AAO65628	Vector contig. TCAR
18	31.8	39.3	9208	15	AAO65629	Vector contig. TCAR
19	31.8	39.3	19001	19	AAZ61793	Traget plasmid Mol
20	31.8	39.3	19035	19	AAZ61794	Traget plasmid Man
21	31.4	38.8	111	14	AAO48066	Human kappa light
22	31.4	38.8	117	14	AAO48067	Human kappa light
23	31.4	38.8	724	20	AAZ90423	Chimeric antibody
24	31.4	38.8	3169	17	AAZ8397	Prte 99 plasmid fr
25	31.2	38.5	779	21	AAZ87973	Humanised anti-IL-
26	31.2	38.5	780	19	AAV5070	Humanised anti-IL-
27	31.2	38.5	780	19	AAV5071	Humanised anti-IL-
28	31.2	38.5	780	20	AAZ90541	Humanised anti-IL-
29	31.2	38.5	780	20	AAZ90542	Anti-human-IL-8 6G
30	31.2	38.5	780	20	AAZ90577	Humanised anti-IL-
31	31.2	38.5	780	21	AAZ65506	6G4-2-V11 light c
32	31.2	38.5	780	21	AAZ65507	GCN4 leucine zipper
33	31.2	38.5	780	21	AAZ65512	Humanised anti-IL-
34	31.2	38.5	780	21	AAZ87967	Humanised anti-IL-
35	31.2	38.5	780	21	AAZ87968	Humanised anti-IL-
36	31.2	38.5	1493	20	AAZ07423	Humanised anti-IL-
37	31.2	38.5	2143	20	AAZ03840	Plasmid pS1130 exp
38	31.2	38.5	2143	21	AAZ53339	Expression cassett
39	31.2	38.5	2143	22	AAZ31463	ps 1130 expression
40	31.2	38.5	2178	13	AAZ25592	Encodes 4D5 Fab Ig
41	31.2	38.5	2178	20	AAZ81689	4D5 Fab molecule c
42	31.2	38.5	6072	19	AAZ71266	VEGF humanised ant
43	31.2	38.5	6072	19	AAZ63493	Rab-display antio
44	31.2	38.5	6127	20	AAZ07474	Mus musculus anti-
45	31.2	38.5	6127	22	AAZ69253	Expression plasmid

ALIGNMENTS

RESULT 1	
ID AAK55755	standard; DNA: 66 BP.
XX	
AC AAK55755:	
XX	
DT 30-JUL-1999	(first entry)
XX	
DE	PCR mutagenic oligo.
XX	
KW	Hinge peptide; cell-associated receptor; dimeric antibody; medicine;
KW	Infectious disease; inflammatory disease; autoimmunity; osteoarthritis;
KW	allergy; atopic disease; asthma; congenital disease; cystic fibrosis;
KW	dermatological disease; psoriasis; neurological; metabolic; cancer;
XX	PCR primer; mutagenic; ss.
XX	
OS	Synthetic.
XX	
PN	WO915549-A2.
XX	
PD	01-APR-1999.
XX	
PF	21-SEP-1998; 98WO-G02851.
XX	
PR	19-SEP-1997; 97GB-0020054.
XX	
PA	(CLUT) CELLTECH THERAPEUTICS LTD.
XX	
PI	Humphreys DP;
XX	
DR	WPI; 1999-244385/20.
XX	
PT	New peptides, useful as hinge regions in proteins for producing
PT	dimeric proteins for use in therapy

XX Example 1: Page 13; 47pp; English.
PS The invention relates to a peptide of 14 defined amino acids which
XX functions as a hinge region in proteins. The peptide has formula (I):
CC NCPPXPYCPPCPAC, where X and Y are neutral aliphatic L-amino acid
CC residues. The new peptide is useful as a hinge region in proteins,
CC especially cell-associated receptors or dimeric antibodies, which are
CC useful in medicine. The new peptides are useful for replacing naturally
CC occurring hinge regions. The proteins are useful for diagnosis and/or
CC treatment of diseases or disorders including infectious diseases:
CC inflammatory disease/autoimmunity e.g. cancer, osteoarthritis; allergic
CC /atropic disease e.g. asthma; congenital disease e.g. cystic fibrosis;
CC dermatological disease e.g. psoriasis; neurological disease and metabolic
CC diseases. The new peptide allows production of divalent antigen binding
CC species e.g. dimeric antibodies, which are non-immunogenic, are not
CC easily cleaved in vivo, are easy to prepare recombinantly and can couple
CC to other effector proteins.
XX
SQ Sequence 66 BP; 28 A; 9 C; 18 G; 11 T; 0 other;

Query Match 63.2%; Score 51.2; DB 20; Length 66;
Best Local Similarity 94.6%; Pred. No. 1.1e-05;
Matches 53; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gagctaccagtaacaaaagcttaataagagagagtggtgagagagaaaaaa 56
|||||
Db 6 gagctaccagtaacaaaagcttaataagagagagtggtgagagagaaaaaa 61

RESULT 2
AAZ50588
ID AAZ50588 standard; DNA; 1630 BP.
XX
XX AAZ50588;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scfv-Ck-Interleukin 2 encoding DNA.
XX
KW HD70: single-chain variable fragment; scfv; 17-1A antigen; human;
KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine;
KW IL-2; interleukin-2; Ck-domain; Kappa light chain constant domain;
KW heteromibody; multifunctional compound; immunoglobulin;
KW cytosatic; immunostimulatory; antileukaemia; diagnosis; prevention;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 39..1613
FT /*tag= a
FT /*product= "HD70scfv-Ck-IL-2 chain"
FT misc_feature 96..842
FT /*tag= b
FT /*label= HD70_scfv
XX
XX WO200006605-A2.
XX
XX 10-FEB-2000.
XX
XX 28-JUL-1999; 99WO-EP05416.
XX
XX 28-JUL-1998; 98EP-0114082.
XX
XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetli F;
PI WPI: 2000-195265/17.
XX
XX P-PSDB; AA144995.
DR

XX New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis
XX
PS Claim 8: Fig 55B; 166pp; English.
XX
CC The patent discloses heteromibodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (polypeptides having
CC different receptor or ligand functions, where further at least two of the
CC different (polypeptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteromibodies have
CC cytosatic, immunostimulatory, antileukemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas.
CC The present sequence is a DNA encoding right chain of a heteromibody
CC comprising HD70 single-chain Fv (scfv) fragment N-terminally linked to
CC human Ck domain (constant domain of immunoglobulin-kappa light chain)
CC which bears at its C-terminus the human inflammatory cytokine
CC interleukin-2 (IL-2). HD70 scfv specifically recognises the human
CC epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.
XX
SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 other;

Query Match 43.5%; Score 35.2; DB 21; Length 1630;
Best Local Similarity 83.3%; Pred. No. 0.42;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 gagctaccagtaacaaaagcttaataagagagagtggtgagagag 48
|||||
Db 1154 gagctccgcgcgtcacaaagcttaacagagagagtggtcagagag 1201

RESULT 3
AAZ50601
ID AAZ50601 standard; DNA; 64 BP.
XX
XX AAZ50601;
XX
DT 23-MAY-2000 (first entry)
XX
DE 5' VHTR66CKSMC primer to obtain anti-CD3 antibody TR66 scfv-fragment.
XX
XX CD3; TR66; antibody; scfv; single-chain Fv fragment; W79; 17-1A antigen;
KW heteromibody; multifunctional compound; immunoglobulin; prevention;
KW cytosatic; immunostimulatory; antileukaemia; diagnosis; constant domain;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200006605-A2.
XX
XX 10-FEB-2000.
XX
XX 28-JUL-1999; 99WO-EP05416.
XX
XX 28-JUL-1998; 98EP-0114082.
XX
XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetli F;
PI WPI: 2000-195265/17.
XX
XX New multifunctional compounds useful for preventing and/or treating
PT

```
PT malignant cell growth and for detection and diagnosis
XX
PS Example 7; Page 67; 166pp: English.
XX
CC The patent discloses heteroantibodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises C $\mu$ -domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (polypeptides having
CC different receptor of ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteroantibodies have
CC cytosolic, immunostimulatory, antileukemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of hematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas.
CC The present sequence is a 5' VHR66CKSAC primer used to amplify
CC the antiCD3scfv-fragment (single-chain Fv fragment) from the DNA
CC encoding specific single chain antibody M79scfv-antiCD3scfv.
CC The antiCD3scfv-fragment is used in the construction of a heteroantibody
CC M79scfvKantiCD3scfv/CD80CH1 comprising the single-chain Fv fragment of
CC murine anti 17-1A antibody M79, the constant domains of human IgG1 heavy
CC chain and kappa light chain, and CD80 molecule. The primer also
CC introduces a restriction cleavage site SacI.
XX
SQ Sequence 64 BP; 15 A; 15 C; 22 G; 12 T; 0 other;
XX
Query Match 41.5%; Score 33.6; DB 21; Length 64;
Best Local Similarity 81.2%; Pred. No. 0.77;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
OY 1 gagctaccagtaacaaagcttaataagagagagtggtgagagag 48
    ||||| || || ||||| ||||| || || ||||| ||||| ||
Db 4 gagctgcgcgtcacaaagagcttcacacagggagagtggtgagag 51
XX
RESULT 4
AAT23297
ID AAT23297 standard; cDNA to mRNA; 548 BP.
XX
AC AAT23297;
XX
DT 30-AUG-1996 (first entry)
XX
DE Human gene signature HUMGS0511.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
```

```
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
XX
PS Claim 1; Page 1335; 2245pp; Japanese.
XX
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in Aat19001-126837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
XX
SQ Sequence 548 BP; 126 A; 134 C; 121 G; 139 T; 28 other;
XX
XX
Query Match 40.5%; Score 32.8; DB 16; Length 548;
Best Local Similarity 75.5%; Pred. No. 1.7;
Matches 40; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
OY 1 gagctaccagtaacaaagcttaataagagagagtggtgagagagaa 53
    ||||| || || ||||| ||||| || || ||||| ||||| ||
Db 289 gagctgcgcgtcacaaagagcttcacacagggagagtggttaagangagagaa 341
XX
RESULT 5
AAQ92546
ID AAQ92546 standard; DNA; 4691 BP.
XX
AC AAQ92546;
XX
DT 11-MAR-1996 (first entry)
XX
DE pComb3 expression vector.
XX
KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;
KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;
KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;
KW combinatorial Fab library; cassette; Pd/cp3; lacZ promoter/operator;
KW ribosome binding site; RBS; pelb leader; spacer; tether sequence;
KW M4; pMT4-3; antibody; ss; cyclic.
XX
OS Synthetic.
XX
PN WO9511317-A1.
XX
PD 27-APR-1995.
XX
PF 19-OCT-1994; 94WO-US11907.
XX
PR 19-SEP-1994; 94US-0308841.
PR 19-OCT-1993; 93US-0139409.
PR 26-APR-1994; 94US-0233619.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Burton DR, Lerner RA;
XX
DR WPI; 1995-170235/22.
XX
PT Synthetic human neutralising monoclonal antibodies to human
PT immunodeficiency virus - used for diagnosis and immuno:therapy of
PT HIV-induced disease
XX
XX
Example 1; Page 185-188; 249pp; English.
```


DR	P-P8DB;AAV56286; AAV56287.
XX	
PT	New virus-like particle or gene delivery vehicle, useful for gene therapy -
XX	
PS	Claim 13; Fig 16; 66pp; English.
XX	
CC	The present invention describes a virus-like particle or gene delivery vehicle comprising a ligand capable of binding to a human amino acid transporter. The method is useful for the target delivery of substances to cells e.g. gene therapy. A human cationic amino acid transporter (hcavt) targeted adenovirus is useful for local applications of adenoviral vector e.g. in patients with restenosis following balloon angioplasty where smooth muscle cells need to be transfected with an adenoviral vector carrying the CENOS cDNA. More efficient transduction of tissues can be carried out therefore resulting in lower multiplicity's of infections that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells. AAZ38737 to AAZ8770, and AAV56284 to AAV56287 represent sequences used in the exemplification of the present invention.
CC	
CC	
SQ	Sequence 5925 BP; 1454 A; 1487 C; 1517 G; 1467 T; 0 other;
XX	
Query Match	39.5%; Score 32; DB 21; Length 5925;
Best Local Similarity	79.2%; Pred. No. 3.7;
Matches	38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY	1 gagctcaccacgaatacaaaaagcttaataatagaaggagagtgttagagg 48
Db	2937 gagtcaccgcgtgacacaagaagctccaacagggagagtgtataaagg 2984
RESULT 8	
AAQ92547	
ID	AAQ92547 standard; DNA; 6166 BP.
XX	
AC	AAQ92547;
XX	
DT	11-MAR-1996 (first entry)
XX	
DE	Expression vector, pPho-TT.
XX	
KW	Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120; 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab; immunoreaction; neutralisation; passive immunotherapy; tetanus toxin; alkaline phosphatase; phoA; ss; cyclic.
KW	
XX	Synthetic.
OS	
XX	
PN	WO9511317-A1.
XX	
PD	27-APR-1995.
XX	
PF	19-OCT-1994; 94WO-US11907.
XX	
PR	19-SEP-1994; 94US-0308841.
PR	19-OCT-1993; 93US-0139409.
ER	26-APR-1994; 94US-0233619.
XX	
PA	(SCRI) SCRIPPS RES INST.
PI	Barbas CF, Burton DR, Lerner RA;
XX	
WP	WI: 1995-170235/22.
XX	
PT	Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-induced disease
XX	
SS	Example 2; Page 193-197; 249pp; English.
XX	This sequence represents the expression vector, pPho-TT which is a

CC	modified version of the phagemid expression vector, pComb3 given in
CC	AA932546. pho-IT provides for the expression of soluble Fabs which are
CC	secreted into the periplasmic space which is regulated from the alkaline
CC	phosphatase (pho) promoter. This plasmid was used within the scope of
CC	the invention to express various mutagenised human Fab's which comprise
CC	heavy and light variable regions which bind to HIV gp120. pho-IT
CC	consists of a DNA molecule having two cassettes to express two soluble
CC	proteins a heavy chain and a light chain. The vector comprises,
CC	operatively linked 5' to 3', a first cassette consisting of the phoA
CC	promoter/operator sequences, an EcoRI restriction site, a ribosome
CC	binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
CC	region, a cloning region bordered by 5' sacI and 3' XbaI restriction
CC	sites, an NcoI restriction site between the two cassettes, and a second
CC	cassette consisting of an expression control RBS, a PelB leader, a human
CC	consensus amino terminus spacer region comprising the sequence EVQLLE,
CC	a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
CC	followed by a SfiI site, expression control stop sequences and a NotI
CC	restriction site. The pho-IT expression vector contains a light
CC	chain stuffer that is 1200 bp in length and a heavy chain stuffer that
CC	is 300 bp in length. The nucleotide sequences of the heavy and light
CC	chain stuffer encode the heavy and light chain variable domains of a
CC	tetanus toxin-specific Fab.
XX	
SQ	Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T; 0 other;
Query Match	39.5%; Score 32; DB 16; Length 6166;
Best Local Similarity	62.5%; Pred. No. 3.8;
Matches	50; Conservative 0; Mismatches 30; Indels 0; Gaps
QY	1 gagctaccagtaacaaaagcttaataagagagagtggtgagagagaaaaaata 60
DB	5203 gagctgcgcgcgcacaaagagcttaacaaaggagagagtgtaattcagataa 5262
QY	61 agaaacatgcataagcaatt 80
DB	5263 gagaggaattaaatgaaat 5282
RESULT	9
AAAT61240	AAAT61240 standard; DNA; 705 BP.
XX	
AC	AAAT61240;
XX	
DT	13-MAY-1997 (first entry)
XX	
DE	Human anti-RSV monoclonal antibody RF-1 light chain DNA.
XX	
KN	Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
KN	RSV; fusion protein; F-protein; VACINE; immunotherapy; therapy;
KM	Epstein Barr virus; immortalisation; recombinant antibody; ss.
KM	
XX	
OS	Homo sapiens.
XX	
FI	Key
FT	Location/Qualifiers
FT	1..60
FT	/*tag= a
FT	61..702
FT	mat-peptide
FT	/*tag= b
XX	
PN	W09640252-A1.
XX	
PD	19-DEC-1996.
XX	
XX	
PF	06-JUN-1996; 96WO-US10070.
XX	
PR	07-JUN-1995; 95US-0488376.
XX	
PA	(IDEC-) IDEC PHARM CORP.
XX	
PI	Brams P, Chamat SS, Heard CJ, Newman RA, Pan L, Walsh EE;

XX WPI: 1997-099892/09.
DR P-PSDB: AAW11638.
XX
XX Human monoclonal antibody specific for respiratory syncytial virus
PT fusion protein - used for the prevention and treatment of RSV
PT Infection
XX
XX Claim 9; Fig 9a; 85pp; English.
XX
XX A DNA sequence (AA61240) codes for a polypeptide (AAW11638) comprising
CC a leader sequence, RFL light chain variable region (see also
CC AAW11634), and human kappa constant region. RFL is a human
CC monoclonal antibody (hMab) specific for the fusion protein of
CC respiratory syncytial virus (RSV). The DNA sequence, in vector
CC NEOSPLA, can be used to produce the light chain construct in
CC transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy
CC and light chain constructs (see also AA61241-42, AA61279) are
CC similarly used. The transfected host cells provide a constant,
CC stable supply of anti-RSV F-protein hMabs for use in the treatment
CC or prevention of RSV infection.
XX
SQ Sequence 705 BP; 178 A; 199 C; 177 G; 151 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 705;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccaglaacaaaagcttaataagagagagtgtga 43
||||| 11 11 ||||| 1111 11 11 ||||| 111111
Db 663 gagctgcgcgcgtcacaaagagcttcacacagggagagtgtga 705

RESULT 10

AA61242
ID AA61242 standard; DNA: 708 BP.

AC AA61242;

XX 13-MAY-1997 (first entry)

XX Human anti-RSV monoclonal antibody RF-2 light chain DNA.

XX Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;

KW RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;

KW Epstein Barr virus; immortalisation; recombinant antibody; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT sig_peptide 1..66
FT /*tag= a
FT mat_peptide 67..708
FT /*tag= b

XX WO9640252-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US10070.

XX 07-JUN-1995; 95US-0488376.

XX (IDEC-) IDEC PHARM CORP.

XX Brans P, Chamat SS, Heard CJ, Newman RA, Pan L;

XX Walsh EE;

XX WPI: 1997-099892/09.

XX P-PSDB: AAW11640.

XX Human monoclonal antibody specific for respiratory syncytial virus

PT fusion protein - used for the prevention and treatment of RSV
PT Infection
XX
XX Claim 9; Fig 11a; 85pp; English.
XX

CC A DNA sequence (AA61242) codes for a polypeptide (AAW11640) comprising
CC a leader sequence, RF2 light chain variable region (see also
CC AAW11636), and human kappa constant region. RF2 is a human
CC monoclonal antibody (hMab) specific for the fusion protein of
CC respiratory syncytial virus (RSV). The DNA sequence, in vector
CC NEOSPLA, can be used to produce the light chain construct in
CC transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy
CC and light chain constructs (see also AA61240-41, AA61279) are
CC similarly used. The transfected host cells provide a constant,
CC stable supply of anti-RSV F-protein hMabs for use in the treatment
CC or prevention of RSV infection.

SQ Sequence 708 BP; 182 A; 196 C; 175 G; 155 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 708;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccaglaacaaaagcttaataagagagagtgtga 43
||||| 11 11 ||||| 1111 11 11 ||||| 111111
Db 666 gagctgcgcgcgtcacaaagagcttcacacagggagagtgtga 708

RESULT 11

AA63530
ID AA63530 standard; DNA: 708 BP.

AC AA63530;

XX 14-NOV-2000 (first entry)

XX DNA encoding a dimeric anti-CD20 light chain polypeptide.

DE

KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;

KW complement system; fcgamma receptor; cytotoxic effector cell;

KW host immune cell; programmed cell death; allergic disorder; cancer;

KW allergic bronchopulmonary aspergillosis; allergic rhinitis;

KW Graves's disease; food allergy; allergic contact dermatitis; cancer;

KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;

KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;

KW diabetes mellitus; candidiasis; aplastic anaemia; ss.

XX Chimeric - Mus sp.

XX Chimeric - Homo sapiens.

OS

XX Key

XX CDS 1..708

XX Location/Qualifiers

FT sig_peptide 1..66
FT /*tag= a
FT /product= "dimeric anti-CD20 light chain polypeptide"

FT misc_feature 67..384
FT /*tag= b
FT /*tag= c
FT /note= "encodes murine anti-human CD20 variable light chain"

FT misc_feature 385..708
FT /*tag= d
FT /note= "encodes human kappa light chain constant region"

XX WO200044788-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US01893.

XX 28-JAN-1999; 99US-0238741.

XX (IDEC-) IDEC PHARM CORP.
 XX
 PA
 PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
 XX
 DR WPI: 2000-514811/46.
 DR P-PSDB: AAB08025.
 XX
 PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
 treatment of cancers, allergic disorders and autoimmune conditions -
 XX
 PS Example 1; Fig 1A-B; 65pp; English.
 XX
 PS The present sequence encodes a dimeric anti-CD20 light chain
 CC polypeptide. The dimeric immunoglobulin is used in the method of the
 CC invention. The specification describes a method for producing an
 CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
 CC engineering a monoclonal antibody to introduce a cysteine molecule
 CC which inhibits formation of intramolecular disulphide bridges between
 CC sister heavy chains on the same antibody molecule. The dimer is a
 CC homodimer or heterodimer that is capable of activating components of the
 CC complement system, and has the ability to activate and kill cells via the
 CC complement cascade. The dimer is also capable of binding to Fc gamma
 CC receptors on cytotoxic effector cells and on host immune cells, and is
 CC capable of initiating programmed cell death. The IgG/IgG dimers may be
 CC used to treat allergic disorders, cancers and autoimmune diseases such
 CC as allergic asthma, allergic bronchopulmonary aspergillosis, allergic
 CC rhinitis, atopic dermatitis, Crohn's disease, Graves' disease, food
 CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell
 CC lymphomas. They may also be used to treat a range of other diseases and
 CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,
 CC pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes,
 CC mellitus, candidiasis and aplastic anaemia. They are also useful for
 CC inducing hyper-cross-linking of membrane antigens and for the
 CC preferential killing of selected cell populations.
 XX
 SQ Sequence 708 BP; 180 A; 196 C; 178 G; 154 T; 0 other;

Query Match 39.3%; Score 31.8; DB 21; Length 708;
 Best Local Similarity 83.7%; Pred. No. 3.3;
 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagcttaataagagagagtggtga 43
 ||||| || || ||||| ||||| || || ||||| |||||
 Db 666 gagctcgccgctcacaaagagcttcacaaagagagagtggtga 708

RESULT 12
 AAT62511
 ID AAT62511 standard; DNA: 720 BP.
 AC AAT62511;
 XX
 DT 25-MAY-1997 (first entry)
 XX
 DE Primatised anti-human B7.1 Antigen antibody 7B6 light chain DNA.
 XX
 KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transectoma; ss.
 XX
 XX Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 XX
 PN W09640878-A1.
 PD 19-DEC-1996.
 PA
 PF 06-JUN-1996; 96WO-US10053.

XX 07-JUN-1995; 95US-0487550.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brawns P, Hanna N, Shetlowsky WS;
 XX
 DR WPI: 1997-108638/10.
 DR P-PSDB: AAW01819.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 PT useful for treating autoimmune disease or graft-versus-host disease
 XX
 PS Claim 9; Fig 9A; 81pp; English.
 XX
 PS 2 DNA sequences (AAT62511 and AAT13847) respectively code for
 CC primatised forms (AAW01819 and AAW01820) of the light and heavy chains
 CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
 CC 7B6. Cloned 7B6 light and heavy variable genes are inserted into
 CC an expression vector (pref. NEO5PLA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
 CC antibodies have also been produced (see also AAW01817-18 and AAW01821-
 CC 22). The primatised antibodies inhibit the B7:CD28 pathway, making
 CC them useful immunosuppressants for the treatment of autoimmune
 CC disorders and graft-versus-host disease.
 XX
 SQ Sequence 720 BP; 178 A; 201 C; 192 G; 149 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 720;
 Best Local Similarity 83.7%; Pred. No. 3.3;
 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagcttaataagagagagtggtga 43
 ||||| || || ||||| ||||| || || ||||| |||||
 Db 678 gagctcgccgctcacaaagagcttcacaaagagagagtggtga 720

RESULT 13
 AAV35486
 ID AAV35486 standard; DNA: 720 BP.
 AC AAV35486;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatised 7B6 light chain DNA.
 XX
 KW Monoclonal antibody; Mb; macaque; light chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; Interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation; ss.
 XX
 OS Macaca fascicularis.
 XX
 FH Key
 FT 1..720 Location/Qualifiers
 FT CDS /*tag= a
 FT /product= 7B6 light chain
 XX
 FN W09819706-A1.
 PD 14-MAY-1998.
 PA
 PF 29-OCT-1997; 97WO-US19906.
 PR 08-NOV-1996; 96US-0746361.
 PA (IDEC-) IDEC PHARM CORP.
 PI Anderson DR, Bräms P, Hanna N;

```
XX WPI: 1998-286601/25.
DR
DR P-PSDB; AAM63762.
XX
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PS cells, e.g. graft rejection or tumours
XX
XX Example 7; Fig 4a; 87pp; English.
XX
XX This sequence encodes a primatized form of the antibody 7B6 light chain
CC from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotype reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other:
SQ
```

```
Query Match          39.3%; Score 31.8; DB 19; Length 720;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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OY 1 gagctcaccagtaacaaaagcttaataagagagagtgta 43
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DB 678 gagctcgccgcgtcacaaagagcttcacagggagagtgta 720
```

```
RESULT 14
AA222287
ID AA222287 standard; DNA; 725 BP.
AC AA222287;
XX
XX 20-DEC-1999 (first entry)
DT
XX Nucleotide sequence of coding region of plasmid pSSpcyHuK.
DE
XX Multimeric protein; immunoglobulin; receptor-ligand complex;
KW hetero-dimeric receptor; trimeric G protein; transgenic; ss.
XX
XX Synthetic.
OS
XX W09949024-A2.
PN
XX 30-SEP-1999.
PD
XX 24-MAR-1999; 99WO-US06506.
PF
XX 25-MAR-1998; 98US-0079249.
PR
XX (PLAN-) PLANET BIOTECHNOLOGY INC.
PA
XX Wycoff KL, Jaiswal SK;
PI
XX WPI: 1999-580446/49.
DR
DR P-PSDB; AAY34096.
XX
XX Producing heterologous multimeric proteins in plants, transformed with
PT
```

```
PT several plasmids expressing polypeptide components, particularly for
PT immunoglobulins
XX
XX Example 1; Fig 5; 42pp; English.
PS
XX
```

```
CC The invention relates to a method for producing heterologous, multimeric
CC proteins in plant cells. The method comprises: (a) transforming the cells
CC with several naked plasmids each encoding some, but not all, of the
CC polypeptide components of the multimeric proteins, and together providing
CC all the polypeptide components; and (b) culturing the cells. The method
CC is used to produce biologically active multimeric proteins particularly
CC immunoglobulins, receptor-ligand complexes, homo- or hetero-dimeric
CC receptors, or trimeric G proteins. This method provides properly
CC associated and assembled multimeric proteins in a fast and efficient
CC process, without the need to cross plants expressing single component of
CC the protein. Transgenic plants containing adjacent and stably integrated
CC plasmids, and their progeny can also express the multimeric proteins. The
CC present sequence represents the nucleotide sequence of the coding region
CC of the plasmid pSSpcyHuK. This plasmid contains a sequence encoding a
CC bean legumin signal peptide and a mouse light chain variable/human kappa
CC constant hybrid with linker sequences.
XX
```

```
SQ Sequence 725 BP; 186 A; 199 C; 169 G; 171 T; 0 other:
```

```
Query Match          39.3%; Score 31.8; DB 20; Length 725;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
OY 1 gagctcaccagtaacaaaagcttaataagagagagtgta 43
      |||||  ||  |||||  |||||  ||  ||  |||||  |||||
DB 679 gagctcgccgcgtcacaaagagcttcacagggagagtgta 721
```

```
RESULT 15
AAF30339
ID AAF30339 standard; CDNA; 6709 BP.
```

```
AC AAF30339;
XX
XX 14-MAY-2001 (first entry)
DT
XX Biotronic plasmid VR1605.
DE
XX
```

```
XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1605;
KW antibody; idiotype; vector; ss.
XX
```

```
OS Chimeric - Cytomegalovirus.
OS Chimeric - Homo sapiens.
OS Chimeric - Bos taurus.
XX
```

```
PN W0200109303-A2.
XX
XX 08-FEB-2001.
PD
```

```
PF 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
PR
```

```
PA (VICA-) VICAL INC.
XX
XX Hermanson GG;
PI
XX WPI: 2001-123319/13.
DR
```

```
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
XX Example 1; Page 97-101; 149pp; English.
PS
XX
```

CC The present sequence is that of bicistronic plasmid VR1605, which
 CC includes the cytomegalovirus immediate-early promoter, enhancer
 CC and 5' untranslated sequences, human immunoglobulin kappa light
 CC and gamma 1 heavy chain constant region DNA (pNegative) coding
 CC sequences, and the transcriptional terminator region polyA and
 CC termination signals from the bovine growth hormone gene. The
 CC vector encodes no immunoglobulin variable regions, and therefore
 CC does not express a functional protein. It serves as a negative
 CC control for vaccination studies involving VR1623 (see AAF1623),
 CC a bicistronic chimeric idiotypic vector. Co-administration of
 CC VR1623 with plasmid VR6200 (see AAF30313) encoding a secreted form
 CC (see AAB20187) of mouse Fms-like tyrosine kinase (Flt-3 ligand),
 CC demonstrated the ability of the present invention to enhance
 CC protection from tumour challenge in a mouse B-cell lymphoma model.
 XX

SQ Sequence 6709 BP; 1675 A; 1798 C; 1660 G; 1576 T; 0 other;

Query Match

Best Local Similarity 39.3%; Score 31.8; DB 22; Length 6709;

Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 gagctaccagtaacaaagcttaataagagagagtggtga 43
 ||||| || || ||||| ||||| || || ||||| |||||
 Db 2158 gagctgcccgtaacaaagcttaacacagcagcagagagtggtga 2200

Search completed: January 5, 2002, 12:49:59
 Job time: 4318 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:45:54 ; Search time 111.65 Seconds
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164.306 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 81

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	4691	4	US-08-591-632-43
2	32	39.5	6166	4	US-08-591-632-51
3	31.8	39.3	705	1	US-08-488-376-16
4	31.8	39.3	705	2	US-08-634-223-16
5	31.8	39.3	705	2	US-08-634-224-16
6	31.8	39.3	705	2	US-08-634-400-16
7	31.8	39.3	705	2	US-08-635-878-16
8	31.8	39.3	705	2	US-08-770-057-16
9	31.8	39.3	705	4	US-09-335-697B-16
10	31.8	39.3	708	1	US-08-488-376-18
11	31.8	39.3	708	2	US-08-634-223-18
12	31.8	39.3	708	2	US-08-634-224-18
13	31.8	39.3	708	2	US-08-634-400-18
14	31.8	39.3	708	2	US-08-635-878-18
15	31.8	39.3	708	2	US-08-770-057-18
16	31.8	39.3	708	4	US-09-335-697B-18
17	31.8	39.3	720	3	US-08-487-550-5
18	31.8	39.3	8540	1	US-08-149-099C-2
19	31.8	39.3	8540	2	US-08-478-967A-2
20	31.8	39.3	8541	1	US-08-476-275-1
21	31.8	39.3	9209	1	US-08-149-099C-3
22	31.8	39.3	9209	1	US-08-476-275-2
23	31.8	39.3	9209	2	US-08-478-967A-3
24	31.8	39.3	18986	2	US-08-819-866-2
25	31.8	39.3	18986	2	US-09-023-715-2
26	31.4	38.8	117	3	US-08-284-516C-34
27	31.4	38.8	117	3	US-08-284-516C-35

ALIGNMENTS

28	31.4	38.8	3169	3	US-08-630-820-5	Sequence 5, Appl
29	31.2	38.5	780	3	US-09-027-449-54	Sequence 54, Appl
30	31.2	38.5	780	3	US-09-027-449-58	Sequence 58, Appl
31	31.2	38.5	780	3	US-09-027-449-65	Sequence 65, Appl
32	31.2	38.5	780	3	US-08-804-444A-54	Sequence 54, Appl
33	31.2	38.5	780	3	US-08-804-444A-58	Sequence 58, Appl
34	31.2	38.5	780	3	US-09-026-985-54	Sequence 54, Appl
35	31.2	38.5	780	3	US-09-026-985-58	Sequence 58, Appl
36	31.2	38.5	780	3	US-09-026-985-65	Sequence 65, Appl
37	31.2	38.5	2143	3	US-09-097-309-5	Sequence 9, Appl
38	31.2	38.5	2143	4	US-09-097-171A-9	Sequence 9, Appl
39	31.2	38.5	2178	1	US-08-463-587A-24	Sequence 24, Appl
40	31.2	38.5	2178	2	US-08-463-667A-2	Sequence 2, Appl
41	31.2	38.5	2178	3	US-08-923-854-24	Sequence 24, Appl
42	31.2	38.5	2178	5	PCT-US91-09133-25	Sequence 25, Appl
43	31.2	38.5	6127	2	US-08-887-352B-1	Sequence 1, Appl
44	31.2	38.5	6127	4	US-09-109-207C-1	Sequence 1, Appl
45	31.2	38.5	6127	4	US-09-296-005-1	Sequence 1, Appl

RESULT 1
US-08-591-632-43
Sequence 43, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbos, Carlos F.
APPLICANT: Burton, Dennis R.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION/DOCKET NUMBER: 34,163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2837
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 4691 base pairs
TYPE: nucleic acid


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RESULT 4
US-08-634-223-16
: Sequence 16, Application US/08634223
: Patent No. 5840298
: GENERAL INFORMATION:
: APPLICANT: BRAMS, Peter
: APPLICANT: CHAMAT, Soulaïma Salim
: APPLICANT: PAN, Li-Zhen
: APPLICANT: WALSH, Edward E.
: APPLICANT: HEARD, Cheryl Janne
: APPLICANT: NEWMAN, Roland Anthony
: TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/634,223
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,376
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-150
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
: US-08-634-223-16

Query Match 39.3%; Score 31.8; DB 2; Length 705;
Best Local Similarity 83.7%; Pred. No. 0.65;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 gagctaccagtaacaaagaagcttataagagagagtgttga 43
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Db 663 gagctgcgcgctcacaagagcgttcaacagggagagctgttca 705

RESULT 5
US-08-634-224-16
: Sequence 16, Application US/08634224
: Patent No. 5866125
: GENERAL INFORMATION:
: APPLICANT: BRAMS, Peter
: APPLICANT: CHAMAT, Soulaïma Salim
: APPLICANT: PAN, Li-Zhen

```

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1 APPLICANT: WALSH, Edward E.
2 APPLICANT: HEARD, Cheryl Janne
3 APPLICANT: NEWMAN, Roland Anthony
4 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
5 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO
6 TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
7 NUMBER OF SEQUENCES: 19
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Burns, Doane, Swecker & Mathis
10 STREET: P. O. Box 1404
11 CITY: Alexandria
12 STATE: Virginia
13 COUNTRY: United States
14 ZIP: 22313-1404
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/634,224
22 FILING DATE:
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/488,376
26 FILING DATE: 07-JUN-1995
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Teskin, Robin L.
29 REGISTRATION NUMBER: 35,030
30 REFERENCE/DOCKET NUMBER: 012712-150
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (703) 836-6620
33 TELEFAX: (703) 836-2021
34 INFORMATION FOR SEQ ID NO: 16:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 705 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: Single
39 TOPOLOGY: linear
40 MOLECULE TYPE: DNA (genomic)
41 FEATURE:
42 NAME/KEY: CDS
43 LOCATION: 1..705
44 US-08-634-224-16
45
46 Query Match 39.3%; Score 31.8; DB 2; Length 705;
47 Best Local Similarity 83.7%; Pred. No. 0.65;
48 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
49
50 QY 1 gagctaccagtaacaaagccttaataagagagagtggtga 43
51 ||||||| || ||||| ||||| || ||||| |||||
52 Db 663 GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGAGAGTGTGGA 705
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54 RESULT 6
55 US-08-634-400-16
56 Sequence 16, Application US/08634400
57 Patent No. 5939068
58 GENERAL INFORMATION:
59 APPLICANT: BRAMS, Peter
60 APPLICANT: CHAMAT, Soulaïma Salim
61 APPLICANT: PAN, Li-Zhen
62 APPLICANT: WALSH, Edward E.
63 APPLICANT: HEARD, Cheryl Janne
64 APPLICANT: NEWMAN, Roland Anthony
65 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
66 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
67 NUMBER OF SEQUENCES: 19
68 METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
69 CORRESPONDENCE ADDRESS:
70 ADDRESSEE: Burns, Doane, Swecker & Mathis
71 STREET: P. O. Box 1404

```


	Query Match	39.3%	Score 31.8;	DB 2;	length 708;
	Best Local Similarity	83.7%	Pred. No. 0.65;		
	Matches 36; Conservative	0;	Mismatches	7;	Indels
					Gaps 0;
QY	1	gagctcaccagttaacaaaagcttcatatagaagaaagtgtca	43		
	666	GAGCTCCGCCCTCACAAAGAGCTTCAACAGGGGAGAGAGTTGA	708		

Query Match	39.3%	Score	31.8	DB	2	Length	708
Best Local Similarity	83.7%	Pred. No.	0.65				
Matches	36	Conservative	0	Mismatches	7	Indels	0
						Gaps	0

RESULT 15
 US-08-770-057-18
 Sequence 18, Application US/08770057
 Patent No. 5958765
 GENERAL INFORMATION:
 APPLICANT: BRAMS, Peter
 APPLICANT: CHAMAT, Soulatima Salim
 APPLICANT: PAN, Li-zhen
 APPLICANT: WALSH, Edward E.
 APPLICANT: HEARD, Cheryl Janne
 APPLICANT: NEWMAN, Roland Anthony
 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
 NUMBER OF INVENTIONS: 1
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Burns, Doane, Swecker & Mathis
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/770,057
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/488,376
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030

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; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..708
; US-08-770-057-18

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Query Match          39.3%; Score 31.8; DB 2; Length 708;
Best Local Similarity 83.7%; Pred. No. 0.65;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 1 gaccacaccagtaacacaaagcttaataagagagagtggtga 43
    |||||  ||  |||||  |||||  ||  ||  |||||  |||||
Db 666 GAGCTCGCCCGTCACACAGAGCTTCACACAGGGGAGAGGTGTGA 708

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Search completed: January 5, 2002, 12:45:56
Job time: 4280 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:15:52 ; Search time 2209.96 Seconds
(without alignments)
393.857 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 81
Sequence: 1 gagctcaccagtaacacaaaa.....gaaactctatagcaatg 81

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_estcl:*
11: gb_estc2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.6	45.2	842	11	BG757770 602714882
2	36.6	45.2	560	10	AI683231 x602b10.x
3	36.6	44.4	844	11	BG685433 602637288
4	36.6	44.4	883	11	BG685152 602637032
5	36.6	44.4	883	11	BG756095 602716589
6	35.6	44.0	313	10	AI815108 w671b04.x
7	35.4	43.7	251	10	AM270172 x072c08.x
8	35.4	43.7	957	11	BG756233 602713544
9	34.4	42.5	302	11	BF834388 CM2-HT096
10	34.4	42.5	367	11	BF174509 MRE3290a
11	34.4	42.5	391	11	H25972
12	34.4	42.5	744	11	BG686771 602650742

13	34.4	42.5	753	11	BG756401	BG756401 602715727
14	34.4	42.5	782	11	BG755364	BG755364 602713920
15	34.4	42.5	841	11	BG758779	BG758779 602711339
16	34.4	42.0	221	10	AM238200	AM238200 x620a06.x
17	34.4	42.0	241	10	BE715579	BE715579 RC4-HT074
18	34.4	42.0	296	10	AI950761	AI950761 w54q03.x
19	34.4	42.0	298	11	BF878071	BF878071 CM2-ET012
20	34.4	42.0	376	10	AM369181	AM369181 I10-HT020
21	34.4	42.0	424	11	BF878112	BF878112 CM2-ET012
22	34.4	42.0	472	11	BF664009	BF664009 602145683
23	34.4	42.0	787	11	BG536224	BG536224 602565445
24	34.4	42.0	1100	11	BF663472	BF663472 602144635
25	33.8	41.7	750	11	BG755394	BG755394 602713951
26	33.8	41.7	864	11	BG686067	BG686067 602638637
27	33.4	41.2	291	10	AM512732	AM512732 x006e12.x
28	33.4	41.2	484	10	AI538356	AI538356 tp64f03.x
29	33.4	41.2	496	10	AI864507	AI864507 w19q04.x
30	33.4	41.2	776	11	BG684027	BG684027 602635634
31	33.4	41.2	852	11	BG745626	BG745626 602723873
32	33.4	41.2	852	11	BG756918	BG756918 602715417
33	33.4	41.2	865	11	BG617325	BG617325 602615353
34	33.2	41.0	414	11	BG381444	BG381444 UI-R-CTO-
35	33.2	41.0	733	11	BG483124	BG483124 602503060
36	33.2	41.0	905	11	BG754585	BG754585 602714527
37	33.2	41.0	988	11	BG756209	BG756209 602713519
38	33.2	40.7	215	10	AM793129	AM793129 CM4-DM000
39	32.8	40.5	190	10	AU165104	AU165104 AU165104
40	32.8	40.5	210	10	BE711101	BE711101 RC3-HT064
41	32.8	40.5	299	10	AA933587	AA933587 cm61h09.s
42	32.8	40.5	458	10	BE719885	BE719885 RC1-HT088
43	32.8	40.5	512	10	AI624583	AI624583 ts30f04.x
44	32.8	40.5	512	10	AA433826	AA433826 zw29d09.t
45	32.8	40.5	547	11	C02031	C02031 HUMGS000511

ALIGNMENTS

RESULT 1
BG757770 842 bp mRNA EST 15-MAY-2001
LOCUS 602714882F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854885 5',
DEFINITION mRNA sequence.
ACCESSION BG757770
VERSION BG757770.1 GI:14068423
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Human.
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rudin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1703 row: d column: 22
High quality sequence stop: 736.
Location/Qualifiers
1. 842
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4854885"
/clone_id="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 883)
TITLE NIH-MGC http://mhc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1622 row: p column: 08
High quality sequence stop: 838.

FEATURES

source

1. 883

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="NIH-MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(5). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT 214 a 260 c 222 g 185 t 2 others
ORIGIN

Query Match 44.4% Score 36; DB 11; Length 883;
Best Local Similarity 80.8%; Pred. No. 1.7e+02;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 gacgtccagtgataaagcttaagagagagtggtgagaggaataa 52
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 675 GACGTCCGCGCTCACAAAGAGCTTCAACAGGAGAGGTGTAGAGGGGGA 726

RESULT 5
LOCUS BG756095 883 bp mRNA EST 15-MAY-2001
DEFINITION 602716589F1 NIH-MGC_48 Homo sapiens cDNA clone IMAGE:4856374 5',
mRNA sequence.
ACCESSION BG756095
VERSION BG756095.1 GI:14066748
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mhc.nci.nih.gov/
AUTHORS 1 (bases 1 to 883)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1CM1707 row: b column: 23

FEATURES High quality sequence stop: 869.
source Location/Qualifiers

1. 883
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="IMAGE:4856374"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGGAG(5). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

BASE COUNT 217 a 252 c 219 g 195 t
ORIGIN

Query Match 44.4% Score 36; DB 11; Length 883;
Best Local Similarity 80.8%; Pred. No. 1.7e+02;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 gacgtccagtgataaagcttaagagagagtggtgagaggaataa 52
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 665 GACGTCCGCGCTCACAAAGAGCTTCAACAGGAGAGGTGTAGAGGGGGA 716

RESULT 6
LOCUS A1815108 313 bp mRNA EST 07-MAR-2000
DEFINITION wR71b04.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2420815 3',
similar to gb:m63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN
); mRNA sequence.
ACCESSION A1815108
VERSION A1815108.1 GI:5426323
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 313)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.dio.llnl.gov/bbrp/image.html
Insert length: 929 Std Error: 0.00
Seq primer: -400P from Gibco.

FEATURES

source

1. 313

Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="NCI-CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site:1: SalI;
Site:2: NotI. Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 71 a 62 c 93 g 87 t
ORIGIN

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	Best Local Similarity	82.0%;	Pred. No. 3.1e+02;		
Matches	41;	Conservative	0;	Mismatches	9; Indels 0; Gaps 0;
Oy	1	gagctcaccacagttaacaaaagcttcaatlagagaagagtggtttaagaagaa	50		
Db	259	gagctcgccctgcacaaaagctttcacacggagggaagagtttagaggagaca	210		

RESULT	7
AM270172	
LOCUS	
DEFINITION	XP_725C08.x1 NCICGAP_bv4 Homo sapiens CDNA clone IMAGE:2745902 3 similar to gb:S49006 IG KAPPA CHAIN C REGION (HUMAN); mRNA sequence.
ACCESSION	AM270172
VERSION	AM270172.1
KEYWORDS	EST.
SOURCE	human.

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 251)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Kitzman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/MLML at:
www-bio.llnl.gov/bdnp/image/image.html

FEATURES

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 250.
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2745902"
/clone_id="NCI_CGAP_Ov40"
/sex="Female"
/tissue_type="endometrialoid ovarian metastasis"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the XbaI sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

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Query Match	43.7%	Score 35.4	DB 10	Length 251
Best Local Similarity	76.4%	Pred. No. 3.6e+02		
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				Indels 0
				Gaps 0
QY	1	gagctcaaccagtaacaaaagccttaataatagaggagagcgttgaggagagaaaaa	55	
		55 GAGCTCGCCCTTCACAAAGAGCTTCACAGGGAGAGTGTAGAGGAGAAAAA	109	
RESULT	8			
GG756233				

LOCUS	BG756233	557 bp	mRNA	15-MAY-2001
DEFINITION	60721354AF1 NIH_MGC_Homo sapiens cDNA clone IMAGE:4853795 5',			
ACCESSION	mRNA sequence.			
VERSION	BG756233			
KEYWORDS	BG756233.1	GI:14066886		
SOURCE	EST.			
ORGANISM	human.			

REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 957)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LUNL at:
<http://image.llnl.gov>
 Plate: L1CMT1700 row: g column: 12
 High quality sequence, stop: 837.

FEATURES	SOURCE	LOCATION/QUALIFIERS
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/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/clone IMAGE:4853795"		
/clone.lib="NH.MGC.48"		
/tissue_type="Primary B-cells from tonsils (cell line)"		
/lab_host="DH10B (phage-resistant)"		
/note="Organ: B-cells; Vector: pGB7. Site:1: XhoI; Site:2: EcoRI. cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(6). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin [University of California, Berkeley] using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NH.MGC library."		
BASE COUNT	240 a	230 g 206 t 1 others
ORIGIN		

Query Match	43.7%	Score 35.4	DB 11	Length 957
Best Local Similarity	79.2%	Pred. No. 2,2e+02		
Matches 42	Conservative 0	Mismatches 11	Indels 0	Gaps 0

Oy	1	gagctcaccagtaacaaaagccttaataagagagagtgcttgagagga	53
db	640	GAGCTCGCCCTTCACAAAGAGCTTCACAAAGGGGAAAGTGTAGAGGAGAGAA	692

RESULT		9	
BFB3438/c			
LOCUS	BFB3438		
DEFINITION	CN2-HT0969-111100-513-g04 HT0969 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BFB3438		
VERSION	BFB3438.1	GI:12184739	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hmo. Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Negai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Grünstein,P.S., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare , M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL MEDLINE COMMENT	<p>Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)</p> <p>Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br</p> <p>This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?PL1-CM2&t2-CM2-Hr0969-111100-513-g04&t3=2000-11-11&t4=1) Seq primer: puc 18 forward High quality sequence start: 5 High quality sequence stop: 302.</p>					
FEATURES	Location/Qualifiers					
SOURCE	1..302 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HR0969" /dev_stage="Adult"					
BASE COUNT	48 a 84 c 83 g 87 t					
ORIGIN						
Query Match	42.5%; Score 34.4; DB 11; Length 302;					
Best Local Similarity	78.8%; Pred.No.5.4e+02;					
Matches 41: Conservative	0; Mismatches 11; Indels 0; Gaps 0;					
OY	1 gagccaccagtaacaaagaacttaatcatgaggaagtcgtttagggaggaaaa 52 Db 65 GAGCTCGGCCGTCACAAAGAGCTTCAACAGGGGAGGAGTGTTAGAGGGAGAGA 14					
RESULT 10						
BF174509	EST 23-MAR-2001					
LOCUS	BF174509 367 bp mRNA					
DEFINITION	MYE3290a Myeloma (MYE) CDNA library Homo sapiens CDNA, mRNA sequence.					
ACCESSION	BF174509					
VERSION	BF174509.1 GI:13440723					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 367) Claudio J.O., Tang,H., Khan,E.M., Vorralla,M., Li,Z., Cukerman,E., Francisco-Pabalan,O., Liew,G.C. and Stewart,A.K.					
TITLE	The transcriptional phenotype of myeloma cells					
JOURNAL COMMENT	Unpublished (2000) Contact: A. Keith Stewart, M.D. Oncology Research University Health Network 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada Tel: (416) 946-4639 Fax: (416) 946-6546 Email: k.stewart@utoronto.ca					
PCR PRIMERS	FORWARD: 5'-GCCAAGTCGCAATTAACCTCACCTACTAAGG-3' BACKWARD: 5'-CCAGTCGAATTGTATATACGACTCATAATAGGCG-3'					
Seq primer:	5'-GAAATTAACCTCACAATAAG-3'.					

FEATURES		Location/Qualifiers	
SOURCE		1. 367	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone_id="myeloma (MYE) CDNA library"	
		/sex="male"	
		/tissue-type="Blood"	
		/cell-type="myeloma"	
		/dev-stage="multiple myeloma"	
		/note="Vector: Lambda Zap Express; site_1: EcoRI; site_2: XhoI; Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-3'-dCTP was added to the nucleotide mixture and a 32P-dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10 ⁶ . Clones from the primary library were randomly selected for single pass sequencing."	
BASE COUNT		96 a 116 c 80 g 74 t 1 others	
ORIGIN			
Query Match		42.5%; Score 34.4; DB 11; Length 367;	
Best Local Similarity		78.8%; Pred. No. 5e+02;	
Matches 41; Conservative		0; Mismatches 11; Indels 0; Gaps 0;	
Oy	1 gagctcaccatatacaaaagcttaataagaggagagcgttgaggaggaataa 52		
	11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11		
Db	133 GAGCTCGCCCTCACAAAGAGCTTCACAGGAGGAGGTGTAAAGAGGAGAA 184		
RESULT 11			
LOCUS		H25972 391 bp mRNA EST 10-JUL-1995	
DEFINITION		y156d07.r1 Soares breast 3Nbstr Homo sapiens CDNA clone IMAGE:162253 5' similar to gp:S49006 IG KAPPA CHAIN C REGION (HUMAN); mRNA sequence.	
ACCESSION		H25972	
VERSION		H25972.1 GI:895095	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE		1 (bases 1 to 391)	
AUTHORS		Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.	
TITLE		The Masnu-Merck EST Project	
JOURNAL		Unpublished (1995)	
COMMENT		Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 664 High quality sequence stops: 307 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 664 Std Error: 0.00	

FEATURES		Location/Qualifiers	
SOURCE		1. 367	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone_id="myeloma (MYE) CDNA library"	
		/sex="male"	
		/tissue-type="Blood"	
		/cell-type="myeloma"	
		/dev-stage="multiple myeloma"	
		/note="Vector: Lambda Zap Express; site_1: EcoRI; site_2: XhoI; Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-3'-dCTP was added to the nucleotide mixture and a 32P-dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10 ⁶ . Clones from the primary library were randomly selected for single pass sequencing."	
BASE COUNT		96 a 116 c 80 g 74 t 1 others	
ORIGIN			
Query Match		42.5%; Score 34.4; DB 11; Length 367;	
Best Local Similarity		78.8%; Pred. No. 5e+02;	
Matches 41; Conservative		0; Mismatches 11; Indels 0; Gaps 0;	
Oy	1 gagctcaccatatacaaaagcttaataagaggagagcgtgtgagaggaataa 52		
	11 11 11 11 11 11 11 11 11 11 11 11 11 11 11		
Db	133 GAGCTCGCCCTCACAAAGAGCTTCACAGGAGGAGGTGTAAAGAGGAGAA 184		
RESULT 11			
LOCUS	H25972	391 bp	mRNA EST 10-JUL-1995
DEFINITION	y156d07.r1 Soares breast 3Nbstr Homo sapiens CDNA clone IMAGE:162253 5' similar to gp:S49006 IG KAPPA CHAIN C REGION (HUMAN); mRNA sequence.		
ACCESSION	H25972		
VERSION	H25972.1 GI:895095		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 391)		
AUTHORS	Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.		
TITLE	The Masnu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 664 High quality sequence stops: 307 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 664 Std Error: 0.00		

Db 663 GAGCTCGCCGCTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 714

RESULT 14
Bg755364 782 bp mRNA EST 15-MAY-2001
LOCUS 602713920F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854173 5',
DEFINITION mRNA sequence.
ACCESSION Bg755364
VERSION Bg755364.1 GI:14066017
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished. (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM1701 row: 9 column: 06
High quality sequence stop: 728.
Location/Qualifiers
1. 782
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4854173"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 194 a 231 c 201 g 156 t

ORIGIN

Query Match 42.5%; Score 34.4; DB 11; Length 782;
Best Local Similarity 78.8%; Pred. No. 3.7e+02;
Matches 41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 gagctaccagtaacaaagctttaataagagagagtgttgagagagaaaa 52
||||| 11 11 11111 11111 11 11111111 11111 11111
Db 687 GAGCTCGCCGCTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 738

RESULT 15
Bg758779 841 bp mRNA EST 15-MAY-2001
LOCUS 602713139F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853553 5',
DEFINITION mRNA sequence.
ACCESSION Bg758779
VERSION Bg758779.1 GI:14069432
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 841)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished. (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM1699 row: m column: 10
High quality sequence stop: 839.
Location/Qualifiers
1. 841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4853553"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 204 a 257 c 208 g 172 t

ORIGIN

Query Match 42.5%; Score 34.4; DB 11; Length 841;
Best Local Similarity 78.8%; Pred. No. 3.6e+02;
Matches 41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 gagctaccagtaacaaagctttaataagagagagtgttgagagagaaaa 52
||||| 11 11 11111 11111 11 11111111 11111 11111
Db 678 GAGCTCGCCGCTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 729

Search completed: January 5, 2002, 12:15:55
Job time: 5639 sec

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